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				LSRKAVSDMLTACKQASFHPDVSDEVRTRALRF GTECTLGYLDLLEHVLVILQKPTPELKQQLAAFS KRVAGAVTELIQAAEAMKGTEWVDPEDPTVIAE TELLGAAASIEAAAKKLEQLKPRAKPKQADETL DFEEQILEAAKSIAAATSALVKSASAAQRELVAQ GKVGSIPANAADDGQWSQGLISAARMVAAATSS LCEAANASVQGHASEEKLISSAKQVAASTAQLL VACKVKADQDSEAMRRLQAAGNAVKRASDNL VRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAA QEEMLKKERELEEARKKLAQIRQQQYKFLPTEL REDEG
3441	A	3	1584	NSARGGVGVRGARAMATVQEKAAALNLSALHS PAHRPPGFSVAQKPFGATYVWSSIINTLQTQVEV KKRRHRLKRHNDCFVGSEAVDVIFSHLIQNKYF GDVDIPRAKVVRVCQALMDYKVFEAVPTKVFG KDKKPTFEDSSCSLYRFTTIPNQDSQLGKENKLY SPARYADALFKSSDIRSASLEDLWENLSLKPANS PHVNISTTLSPQVINEVWQEETIGRLLQLVDLPLL DSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGIL KAYSDSQEDEWLSAAIDCLEYLPDQMVVEISRSF PEQPDRTDLVKELLFDAIGRYYSSREPLLNHLSD VHNGIAELLVNGKTEIALEATQLLLKLLDFQNRE EFRRLLYFMAVAANPSEFKLQKESDNRMVVKRI FSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKI PGTL\HKIVS\VK\LMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSAKE KKK\LLGQFYKCHPDIFIEHFGD
3442	A	160	822	SPASGHCRLNGAAVAMFGCLVAGRLVQTAAQQ VAEDKFVFDLPDYESINHVVVFMLGTIPFPEGMG GSVYFSYPDSNGMPVVWQLLGFVTNGKPSAIFKIS GLKSGEGSQHPFGAMNIVRTPSVAQIGISVELLDS MAQQTPVGNAAVSSVDSFTQFTQKMLDNFYNF ASSFAVSQ/VPDDTQ/RPSEMFIPANVVLKWYENF QRRTSTEPSLLENIIWIKINF
3443	A	3	1373	SWHVRRRWLEATMAGGMKVAVSPAVGPGPWG SGVGGGGTVRLLLILSGCLVYGTAETDVNVVML QESQVCEKRASQQFCYTNVLIPQWHDIWTRIQIR VNSSRLVRVTQVENEEKLKELEQFSIWNFFSSFL KEKLNDTYVNVGLYSTKTCLKVEIIEKDTKYSVI VIRRFDPKLFLVFLLGLMLFFCGDLLSRSQIFYYS TGMTVGIVASL\LIIIFILSKFMPKKSPIYVILVGGW SFSLYLIQLVFKNLQEIWRCYWQYLLSYVLTVGF MSFAVCYKYGPLENERSINLLTWTLQLMGLCFM YSGIQIPHIALAIIIIALCTKNLEHPIQWLYITCRKV CKGAEKPVPPRLLTEEEYRIQGEVETRKALEELR EFCNSPDCSAWKTVSRIQSPKRFADFVEGSSHLT PNEVSVHEQEYGLGSIIAQDEIYEEASSEEEDSYS RCPAITQNNFLT
3444	A	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLG EPG\GSLGWVLPNTAMKKKVLLMGKSGSGKTS MRSIIFANYIARDTRRLGATILDRIHSLQINSSLST YSLVDSVGNTKTFDVEHSHVRFLGNLVLNLWDC GGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESR ELEKDMHYYQSCLEAILQNSPDAKIFCLVHKMD LVQEDQRDLIFKEREEDLRRLSRPLECSCFRTSIW

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				DETLYKAWSSIVYQLIPNVQQLEMNLRNFAEIIE ADEVLLFERATFLVISHYQCKEQRDAHRFEKISNI IKQFKLSCSKLAASFQSMEVRNSNFAAFIDIFTSN TYVMVVMSDPSIPSAATLINIRNARKHFEKLERV DGPKQCLLMR
3445	A	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLG EPG\GSLGWVLPNTAMKKKVLLMGKSGSGKTS MRSIIFANYIARDTRRLGATILDRIHSLQINSSLST YSLVDSVGNTKTFDVEHSHVRFLGNLVLNLWDC GGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESR ELEKDMHYYQSCLEAILQNSPDAKIFCLVHKMD LVQEDQRDLIFKEREEDLRRLSRPLECSCFRTSIW DETLYKAWSSIVYQLIPNVQQLEMNLRNFAEIIE ADEVLLFERATFLVISHYQCKEQRDAHRFEKISNI IKQFKLSCSKLAASFQSMEVRNSNFAAFIDIFTSN TYVMVVMSDPSIPSAATLINIRNARKHFEKLERV DGPKQCLLMR
3446	A	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLG EPG\GSLGWVLPNTAMKKKVLLMGKSGSGKTS MRSIIFANYIARDTRRLGATILDRIHSLQINSSLST YSLVDSVGNTKTFDVEHSHVRFLGNLVLNLWDC GGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESR ELEKDMHYYQSCLEAILQNSPDAKIFCLVHKMD LVQEDQRDLIFKEREEDLRRLSRPLECSCFRTSIW DETLYKAWSSIVYQLIPNVQQLEMNLRNFAEIIE ADEVLLFERATFLVISHYQCKEQRDAHRFEKISNI IKQFKLSCSKLAASFQSMEVRNSNFAAFIDIFTSN TYVMVVMSDPSIPSAATLINIRNARKHFEKLERV DGPKQCLLMR
3447	A	1	2930	VLLGPLWDKLSTADHPVIVTMASKRKSTTPCMIP VKTVVLQDASMEAQPAETLPEGPQQDLPPEASA ASSEAAQNPSSTDGSTLANGHRSTLDGYLYSCK YCDFRSHDMTQFVGHMNSEHTDFNKDPTFVCSG CSFLAKTPEGLSLHNATCHSGEASFVWNVAKPD NHVVVEQSIPESTSTPDLAGEPSAEGADGQAEIIIT KTPIMKIMKGKAEAKKIHTLKENVPSQPVGEALP KLSTGEMEVREGDHSFINGAVPVRQASASSAKN PHAANGPLIGTVPVLPAGIAQFLSLQQQPPVHAQ HHVHQPLPTAKALPKVMIPLSSIPTYSAAMDSNS FLKNSFHKFPYPTKAELCYLTVVTKYPEEQLKIW FTAQRLKQGISWSPEEIEDARKKMFNTVIQSVPQ PTITVLNTPLVASAGNVQHLIQAALPGHVVGQPE GTGGGLLVTQPLMANGLQATSSPLPLTVTSVPK QPGVAPINTVCSNTTSAVKVVNAAQSLLTACPSI TSQAFLDASIYKNKKSHEQLSALKGSFCRNQFPG QSEVEHLTKVTGLSTREVRKWFSDRRYHCRNLK GSRAMIPGDHRSIIIDSVPEVSFSPSSKVPEVTCIPT TATLATHPSAKRQSWHQTPDFTPTKYKERAPEQ LRALESSFAQNPLPLDEELDRLRSETKMTRREIDS WFSERRKKVNAEETKKAEENASQEEEEAAEDEG GEEDLASELRVSGENGSLEMPSSHILAERKVSPIK INLKNLRVTEANGRNEIPGLGACDPEDDESNKLA EQLPGKVSCKKTAQQRHLLRQLFVQTQWPSNQD YDSIMAQTGLPRPEVVRWFGDSRYALKNGQLK WYEDYKRGNFPPGLLVIAPGNRELLQDYYMTHK

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				MLYEEDLQNLCDKTQMSSQQVKQWFAEKMGEE TRAVADTGSEDQGPGTGELTAVHKGMGDTYSE VSENSESWEPRVPEASSEPFD\TSSPQAGRQLETD
3448	A	2	1324	FVARAEKGFRTREAHLLQVAGVGTGLQNGASLS GLASGVMAQRAFPNPYADYNKSLAEGYFDAAG RLTPEFSQRLTNKIRELLQQMERGLKSADPRDGT GYTGWAGIAVLYLHLYDVFGDPAYLQLAHGYV KQSLNCLTKRSITFLCGDAGPLAVAAVLYHKMN NEKQAEDCITRLIHLNKIDPHAPNEMLYGRIGYIY ALLFVNKNFGVEKIPQSHIQQICETILTSGENLAR KRNFTAKSPLMYEWYQEYYVGAAHGLAGIYYY LMQPSLQVSQGKLHSLVKPSVDYVCQLKFPSGN YPPCIGDNRDLLVHWCHGAPGVIYMLIQAYKVF· R/EREKYLC\DAYQCADVIWQYGLLKKGYGLCY\ GSAGNAYAFLTLYNLTQDMKYLYRACKFAEWC LEYGEHGCRTPDTPFSLFEGMAGTIYFL\ADLLFP TKAR\FPAFEL
3449	A	3	2389	SRHVTGAARSPSRAGPSDPPAMGDEDDDESCAV ELRITEANLTGHEEKVSVENFELLKVLGTGAYGK VFLVRKAGGHDAGKLYAMKVLRKAALVQRAK TQEHTRTERSVLELVRQAPFLVTLHYAFQTDAKL HLILDYVSGGEMFTHLYQRQYFKEAEVRVYGGE IVLALEHLHKLGIIYRDLKLENVLLDSEGHIVLTD FGLSKEFLTEEKERTFSFCGTIEYMAPEIIRSKTGH GKAVDWWSLGILLFELLTGASPFTLEGERNTQAE VSRRILKCSPPFPPRIGPVAQDLLQRLLCKDPKKR LGAGPQGAQEVRNHPFFQGLDWVALAARKIPAP FRPQIRSELDVG\NFAEEFTRLEPVYSPPGQ\PPPG DPRIFQGYSFVAPSILFDHNNAVMTDGLEAPGAG DRPGRAAVARSAMMQDSPFFQQYELDLREPALG QGSFSVCRRCRQRQSGQEFAVKILSRRLEANTQR EVAALRLCQSHPNVVNLHEVHHDQLHTYLVLEL LRGGELLEHIRKKRHFSESEASQILRSLVSAVSFM HEEAGVVHRDLKPENILYADDTPGAPVKIIDFG/F SPRLRPQSPGVPMQTPSFTLQYAAPELLAQQGYD ESCDLWSLGVILY\MMLSGQAPFQGASGQGGQS QAAEIMCKIREGRFSLDGEAWQGVSEEAKELVR GLLTVDPAKRLKLEGLRGSSWLQDGSARSSPPLR TPDVLESSGPAVRSGLNATFMAFNRGKREGFFLK SVENAPLAKRRKQKLRSATASRRGSPAPANPGR APVASKGAPRRANGPLPPS
3450	A	201	1705	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDS EDRSDSRAAQPAHDSGHGDDESPSTSSGTAGTSS VPELPGFYFDPEKKRYFRLLPGHNNCNPLTKESIR QKEMESKRLRLLQEEDRRKKIARMGFNASSMLR KSQLGFLNVTNYCHLAHELRLSCMERKKVQIRS MDPSALASDRFNLILADTNSDRLFTVNDVTVGGS KYGIINLQSLKTPTLKVFMHENLYFTNRKV\NSV CWASLNHLDSHILLCLMGLAETPGCATLLPASLF VNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQA NNCFSTGLSRRVLLTNVVTGHRQSFGTNSDVLA QQFALMAPLLFNGCRSGEIFAIDLRCGNQGKGW KATRLFHDSAVTSVRILQDEQYLMASDMAGKIK LWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGI LVAVGQDCYTRIWSLHDARLLRTIPSPYPASKAD

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				IPSVAFSSRLGGSRGAPGLLMAVGQDLYCYSYS
3451	A	19	6033	LLSAMLSHGAGLALWITLSLLQTGLAEPERCNFT LAESKASSHSVSIQWRILGSPCNFSLIYSSDTLGA ALCPTFRIDNTTYGCNLQDLQAGTIYNFKIISLDE ERTVVLQTDPLPPARFGVSKEKTTSTGLHVWWT PSSGKVTSYEVQLFDENNQKIQGVQIQESTSWNE YTFFNLTAGSKYNIAITAVSGGKRSFSVYTNGST VPSPVKDIGISTKANSLLISWSHGSGNVERYRLM LMDKGILVHGGVVDKHATSYAFHGLSPGYLYNL TVMTEAAGLQNYRWKLVRTAPMEVSNLKVTND GSLTSLKVKWQRPPG\NVDSYNITLSHKGTIKESR VLAPWIT\ETHFKELVPGRLY\QVTCSAVSLGELS AQKM\AVGRTFPDKVANLEANNNGRMRSLVVS WSPPAGDWEQYRILLFNDSVVLLNITVGKEETQ YVMDGTGLVPGRQYEVEVIVESGNLKNSERCQG RTVPLAVLQLRVKHANETSLSIMWQTPVAEWEK YIISLADRDLLLIHKSLSKDAKEFTFTDLVPGRKY MATVTSISGDLKNSSSVKGRTVPAQVTDLHVAN QGMTSSLFTNWTQAQGDVEFYQVLLIHENVVIK NESISSETSRYSFHSLKSGSLYSVVVTTVSGGISSR QVVVEGRTVPSSVSGVTVNNSGRNDYLSVSWLL APGDVDNYEVTLSHDGKVVQSLVIAKSVRECSF SSLTPGRLYTVTITTRSGKYENHSFSQERTVPDKV QGVSVSNSARSDYLRVSWVHATGDFDHYEVTIK NKNNFIQTKSIPKSENECVFVQLVPGRLYSVTVT TKSGQYEANEQGNGRTIPEPVKDLTLRNRSTEDL HVTWSGANGDVDQYEIQLLFNDMKVFPPFHLVN TATEYRFTSLTPGRQYKILVLTISGDVQQSAFIEG FTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDS YTVSAFRHSQKVDSQTIPKHVFEHTFHRLEAGEQ YQIMIASVSGSLKNQINVVGRTVPASVQGVIADN AYSSYSLIVSWQKAAGVAERYDILLLTENGILLR NTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFS KEAQTEGRTVPAAVTDLRITENSTRHLSFRWTAS EGELSWYNIFLYNPDGNLQERAQVDPLVQSFSFQ NLLQGRMYKMVIVTHSGELSNESFIFGRTVPASV SHLRGSNRNTTDSLWFNWSPASGDFDFYELILYN PNGTKKENWKDKDLTEWRFQGLVPGRKYVLW VVTHSGDLSNKVTAESRTAPSPPSLMSFADIANT SLAITWKGPPDWTDYNDFELQWLPRDALTVFNP YNNRKSEGRIVYGLRPGRSYQFNVKTVSGDSWK TYSKPIFGSVRTKPDKIQNLHCRPQNSTAIACSWI PPDSDFDGYSIECRKMDTQEVEFSRKLEKEKSLL NIMMLVPHKRYLVSIKVQSAGMTSEVVEDSTIT MIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFS DTNGAVKYFTVVVREADGSDELKPEQQHPLPSY LEYRHNASIRVYQTNYFASKCAENPNSNSKSFNI KLGAEMESLGGKCDPTQQKFCDGPLKPHTAYRI SIRAFTQLFDEDLKEFTKPLYSDTFFSLPITTESEP LFGAIEGVSAGLFLIGMLVAVVALLICRQKVSHG RERPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIK INQFEGHFMKLQADSNYLLSKEYEELKDVGRNQ SCDIALLPENRGKNRYNNILPYDATRVKLSNVDD DPCSDYINASYIPGNNFRREYIVTQGPLPGTKDDF WKMVWEQNVHNIVMVTQCVEKGRVKCDHYW

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				PADQDSLYYGDLILQMLSESVLPEWTIREFKICGE EQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVR TVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDR ILQQLDSKDSVDIYGAV\HDLRLHRVHMVQTEC QYVYLHQCVRDVLRARKLRSEQENPLFPIYENV NPEYHRDPVYSRH
3452	A	63	1073	FFRSSSDNGSPIRQYE/HSTPAHQGPVMGLEGKS/ ARNSQLRIVLVGKTGAGKSATGNSILGRKVFHSG TAAKSITKKCEKRSSSWKETELVVVDTPGIFDTE VPNAETSKEIIRCILLTSPGPHALLLVVPLGRYTEE EHKATEKILKMFGERARSFMILIFTRKDDLGDTN LHDYLREAPEDIQDLMDIFGDRYCALNNKATGA EQEAQRAQLLGLIQRVVRENKEGCYTNRMYQR AEEEIQKQTQAMQELHRVELEREKARIREEYEEK IRKLEDKVEQEKRKKQMEKKLAEQEAHYAVRQ QRARTEVESKDGILELIMTALQIASFILLRLFAED
3453	A	2674	514	GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAV DKKVDCPRLCTCEIRPWFTPRSIYMEASTVDCND LGLLTFPARLPANTQILLLQTNNIAKIEYSTDFPV NLTGLDLSQNNLSSVTNINGKKMPQLLSVYLEEN KLTELPEKCLSELSNLQELYINHNLLSTISPGAFIG LHNLLRLHLNSNRLQMINSKWFDALPNLEILMIG ENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNAL VGLENLESISFYDNRLIKVPHVALQKVVNLKFLD LNKNPINRIRRGDFSNMLHLKELGINNMPELISID SLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKL ESLMLNSNALSALYHGTIESLPNLKEISIHSNPIRC DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQ NVRQVHFRDMMEICLPLIAPESFPSNLNVEAGSY VSFHCRATA\EPQPEIYWITPSGQKLLPNTLTDKF YVHSEGTLDINGVTPKEGGLYTCIATNLVGADLK SVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSW KASSKILKSSVKWTAFVKTENSHAAQSARIPSDV KVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVT TKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVIC LISCLSPEMNCDGGHSYVRNYLQKPTFALGELYP PLINLWEAGKEKSTSLKVKATVIGLPTNMS
3454	A	1844	244	ERYLFATYVAPSATLDIGLQQEKKKEIYMKIQPP FEDLFDTAEEYILLLLLEPWTKMVKSDQIAYKKV ELVEETRQLDSTYFRKLQALHKETFSKKAEDTTC EIGTGILSLSNVSKRTEYWDNVPAEYKHFKFSDL LNNKLEFEHFRQFLETHSSSMDLMCWTDIEQFRR ITYRDRNQRKAKSIYIKNKYLNKKYFFGPNSPAS LYQQNQVMHLSGGWGKILHEQLDAPVLVEIQK HVQNRLENVWLPLFLASEQFAARQKIKVQMKDI AEELLLQKAEKKIGVWKPVESKWISSSCKIIAFRK ALLNPVTSRQFQRFVALKGDLLENGLLFWQEVQ KYKDLCHSHCDESVIQKKITTIINCFINSSIPPALQI DIPVEQAQKIIEHRKELGPYVFREAQMTFLGVMF KFWPQFCEFRKNLTDENIMSVLERRQEYNKQKK KLAVL/QNDEKSGKDGIKQYANTSVPAIKTALLS DSFLGLQPYGRQPTWCYSKYIEALEQERILLKIQE ELEK\SCLQACNLSQILRLALQLCL
3455	A	228	3330	APTAQAMMSFGGADALLGAPFAPLHGGGSLHY ALARKGGAGGTRSAAGSSSGFHSWTRTSVSSVS

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				ASPSRFRGAGAASSTDSLDTLSNGPEGCMVAVA TSRSEKEQLQALNDRFAGYIDKVRQLEAHNRSLE GEAAALRQQQAGRSAMGELYEREVREMRGAVL RLGAARGQLRLEQEHLLEDIAHVRQRLDDEARQ REEAEAAARALARFAQEAEAARVDLQKKAQAL QEECGYLRRHHQEEVGELLGQIQGSGAAQAQM QAETRDALKCDVTSALREIRAQLEGHAVQSTLQ SEEWFRVRLDRLSEAAKVNTDAMRSAQEEITEY RRQLQARTTELEALKSTKDSLERQRSELEDRHQA DIASYQEAIQQLDAELRNTKWEMAAQLREYQDL LNVKMALDIEIAAYRKLLEGEECRIGFGPIPFSLP EGLPKIPSVSTHIKVKSEEKIKVVEKSEKETVIVEE QTEETQVTEEVTEEEDKEAKEEEGKEEEGGEEEE AEGGEEETKSPPAEEAASPEKEAKSPVKEEAKSP AEAKSPEKEEAKSPAEVKSPEKAKSPAKEEAKSP PE\AKSPEKDGKQNFQAEVKSPEKAKSPAKEEAK SPAEAKSPEKAKSPVKEEAKSPAEAKSPVKEEAK SPAEVKSPEKAKSPTKEE\AKSPEKAKSPEKAKSP EKEEAKSPEKAKSPVKAEAKSPEKAKSPVKAEA KSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKA KSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKA KTLDVKSPEAKTPAKEEARSPADKFPEKAKSPVK EEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPV KEEEKPQEVKVKEPPKKAEEEKAPATPKTEEKK DSKKEEAPKKEAPKPKVEEKKEPAVEKPKESKV EAKKEEAEDKKKVPTPEKEAPAKVEVKEDAKPK EKTEVAKKEPDDAKAKEPSKPAEKKEAAPEKKD TKEEKAKKPEEKPKTEAKAKEDDKTLSKEPSKP KAEKAEKSSSTDQKDSKPPEKATEDKAAKGK
3456	A	258	1463	YLSFIPGHASKSAPMNGHCFAENGPSQKSSLPPLL IPPSENLGPHEEDQVVCGFKKLTVNGVCASTPPL TPIKNSPSLFPCAPLCERGSRPLPPLPISEALSLDDT DCEVEFLTSSDTDFLLEDSTLSDFKYDVPG\RRSF RGCGQINYAYFDTPAVSAADLSYVSDQNG\GVP DPNPPPPQTHRRLRRSHSGPAGSFNKPAIRISNCCI HRASPNSDEDKPEVPPRVPIPPRPVKPDYRRWSA EVTSSTYSDEDRPPKVPPREPLSPSNSRTPSPKSLP SYLNGVMPPTQSFAPDPKYVSSKALQRQNSEGS ASKVPCILPIIENGKKVSSTHYYLLPERPPYLDKY EKFFREAKKKNGGAQIQPLPADCGISSATEKPDS KTKMDLGGHVKRKHLSYVGTP
3457	A	2	4869	FILSSSSSASSEHFHHHYSFGNWWPGSFKGHRMS LPFYQRCHQHYDLSYRNKDVRSTVSHYQREKKR SAVYTQGSTAYSSRSSAAHRRESEAFRRASASSS QQQASQHALSSEVSRKAASAYDYGSSHGLTDSS LLLDDYSSKLSPKPKRAKHSLLSGEEKENLPSDY MVPIFSGRQKHVSGITDTEEERIKEAAAYIAQRNL LASEEGITTPKQSTASKQTTASKQSTASKQSTASK QSTASRQSTASRQSVVSKQATSALQQEETSEKKS RKVVIRGKAERLSLRKTLEETETYHAKLNEDHLL HAPEFIIKPRSHTVWEKENVKLHCSIAGWPEPRV TWYKNQVPINVHANPGKYIIESRYGMHTLEINAC DFEDTAQYRASAMNVKGELSAYASVVVKRYKG EFDETRFHAGASTMPLSFGVTPYGYASRFEIHFD DKFDVSFGREGETMSLGCRVVITPEIKHFQPEIQ

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				WYRNGVPLSPSKWVQTLWSGERATLTFSHLNKE DEGLYTIRVRMGEYYEQYSAYVFVRDADAEIEG APAAPLDVKCLEANKDYIIISWKQPAVDGGSPIL GYFIDKCEVGTDSWSQCNDTPVKFARFPVTGLIE GRSYIFRVRAVNKMGIGFPSRVSEPVAALDPAEK ARLKS/PPLSTLDWT\VIVTEEEPSEGIVPGPPTDLS VTEATRSYVVLSWKPPGQRGHEGIMYFVEKCEA GTENWQRVNTELPVKSPRFALFDLAEGKSYCFR VRCSNSAGVGEPSEATEVTVVGDKLDIPKAPGKI IPSRNTDTSVVVSWEESKDAKELVGYYIEANVA GSGKWEPCNNNPVKTHRFTCHGLVTGQSYIFRV RAVNAAGLSEYSQDSEAIEVKAAIAPPSPPCDITC LESFRDSMVLGWKQPDKIGGAEITGYYVNYREV IDGVPGKWREANVKAVSEEAYKISNLKENMVY QFQVAAMNMAGLGAPSAVSECFKCEEWTIAVP GPPHSLKCSEVRKDSLVLQWKPPVHSGRTPVTG YFVDLKEAKAKEDQWRGLNEAAIKNVYLKVRG LKEGVSYVFRVRAINQAGVGKPSDLAGPVVAET RPGTKEVVVNVDDDGVISLNFECDKMTPKSEFS WSKDYVSTEDSPRLEVESKGNKTKMTFKDLGM DDLGIYSCDVTDTDGIASSYLIDEEELKRLLALSH EHKFPTVPVKSELAVEILEKGQVRF\WMQAEKLS GNAKVNYIFNEKGIFEGPKYKMHIDRNTGIIEMF MEKLQDEDEGTYTFQLQDGKATNHSTVVLVGD VFKKLQKEAEFQRQEWIRKQGPHFVEYLSWEVT GECNVLLKCKVANIKKETHIVWYKDEREISVDE KHDFKDGICTLLITEFSKKDAGIYEVILKDDRGK DKSRLKLVDEAFKELMMEVCKKIALSATDLKIQ STAEGIQLYSFVTYYVEDLKVNWSHNGSAIRYSD RVKTGVTGEQIWLQINEPTPNDKGKYVMELFDG KTGHQKTVDLSGQAYDEAYAEFQRLKQAAIAEK NRARVLGGLPDVVTIQEGKALNLTCNVWGDPPP EVSWLKNEKALASDDHCNLKFEAGRTAYFTING VSTADSGKYGLVVKNKYGSETSDFTVSVFIPEEE ARMAALESLKGGKKAK
3458	A	3963	827	LSRSSSDNNTNTLGRNVMSTATSPLMGAQSFPNL TTPGTTSTVTMSTSSVTSSSNVATATTVLSVGQS LSNTLTTSLTSTSSESDTGQEAEYSLYDFLDSCRA STLLAELDDDEDLPEPDEEDDENEDDNQEDQEY EEVMILRRPSLQRRAGSRSDVTHHAVTSQLPQVP AGAGSRPIGEQEEEEYETKGGRRRTWDDDYVLK RQFSALVPAFDPRPGRTNVQQTTDLEIPPPGTPHS ELLEEVECTPSPRLALTLKVTGLGTTREVELPLTN FRSTIFYYVQKLLQLSCNGNVKSDKLRRIWEPTY TIMYREMKDSDKEKENGKMGCWSIEHVEQYLG TDELPKNDLITYLQKNADAAFLRHWKLTGTNKS IRKNRNCSQLIAAYWDLG\EHGTK\SGLNQGAIST LQSSDILNLTKEQPQAKAGNGQNSCGVEDVLQL LRILYIVASDPYSRISQEDGDEQPQFTFPPDEFTS/ KKITTKILQQIEEPLALASGALPDWCEQLTSKCPF LIPFETRQLYFTCTAFGASRAIVWLQNRREATVE RTRTTSSVRRDDPGEFRVGRLKHERVKVPRGESL MEWAENVMQIHADRKSVLEVEFLGEEGTGLGPT LEFYALVAAEFQRTDLGAWLCDDNFPDDESRHV DLGGGLKPPGYYVQRSCGLFTAPFPQDSDELERI

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				TKLFHFLGIFLAKCIQDNRLVDLPISKPFFKLMCM GDIKSNMSKLIYESRGDRDLHCTESQSEASTEEG HDSLSVGSFEEDSKSEFILDPPKPKPPAWFNGILT WEDFELVNPHRARFLKEIKDLAIKRRQILSNKGL SEDEKNTKLQELVLKNPSGSGPPLSIEDLGLNFQF CPSSRIYGFTAVDLKPSGEDEMITMDNAEEYVDL MFDFCMHTGIQKQMEAFRDGFNKVFPMEKLSSF SHEEVQMILCGNQSPSWAAEDIINYTEPKLGYTR DSPGFLRFVRVLCGMSSDERKAFLQFTTGCSTLP PGGLANLHPRLTVVRKVDATDASYPSVNTCVHY LKLPEYSSEEIMRERLLAATMEKGFHLN
3459	A	88	603	SCGPRGLASLGLGFSGRCDDQNKGRS\DGPEAQA EACSGERTYQELLVNQNPIAQPLASRRLTRKLYK CIKKAVKQKQIRRGVKEVQKFVNKGEKGIMVLA GDTLPIEVYCHLPVMCEDRNLPYVYIPSKTDLGA AAGSKRPTCVIMVKPHEEYQEAYDECLEEVQSL PLPL
3460	A	139	1997	QVTNMSDKSELKAELERKKQRLAQIREEKKRKE EERKKKETDQKKEAVAPVQEESDLEKKRREAEA LLQSMGLTPESPIVPPPMSPSSKSVSTPSEAGSQD SGDGAVGSRRGPIKLGMAKITQVDFPPREIVTYT KETQTPVMAQPKEDEEEDDDVVAPKPPIEPEEEK TLKKDEEN\DSKAPPHELTEEEKQQILHSEEFLSFF DHSTRIVERALSEQINIFFDYSGRDF/ENDKEGEIQ AGAKLSLNRQFF\DER\WSKASGWVSCLDWSSQ YP\ELLVASYNNNEDAPHEPDGVALVWNMKYK KTTPEYVFHCQSAVMSATFAKFHPNLVVGGTYS GQIVLWDNRSNKRTPVQRTPLSAAAHTHPVYCV NVVGTQNAHNLISISTDGKICSWSLDMLSHPQDS MELVHKQSKAVAVTSMSFPVGDVNNFVVGSEE GSVYTACRHGSKAGISEMFEGHQGPITGIHCHAA VGAVDFSHLYVTSSFDWTVKLWTTKNNKPLYSF EDNAGYVYDVMWSPTHPALFACVDGMGRLDL WNLNNDTEVPTASISVEGNPALNRVRWTHSGRE IAVGDSEGQIVIYDVGEQIAVPRNDEWARFGRTL AEINANRADAEEEAATRIPA
3461	A	139	1997	QVTNMSDKSELKAELERKKQRLAQIREEKKRKE EERKKKETDQKKEAVAPVQEESDLEKKRREAEA LLQSMGLTPESPIVPPPMSPSSKSVSTPSEAGSQD SGDGAVGSRRGPIKLGMAKITQVDFPPREIVTYT KETQTPVMAQPKEDEEEDDDVVAPKPPIEPEEEK TLKKDEEN\DSKAPPHELTEEEKQQILHSEEFLSFF DHSTRIVERALSEQINIFFDYSGRDF/ENDKEGEIQ AGAKLSLNRQFF\DER\WSKASGWVSCLDWSSQ YP\ELLVASYNNNEDAPHEPDGVALVWNMKYK KTTPEYVFHCQSAVMSATFAKFHPNLVVGGTYS GQIVLWDNRSNKRTPVQRTPLSAAAHTHPVYCV NVVGTQNAHNLISISTDGKICSWSLDMLSHPQDS MELVHKQSKAVAVTSMSFPVGDVNNFVVGSEE GSVYTACRHGSKAGISEMFEGHQGPITGIHCHAA VGAVDFSHLYVTSSFDWTVKLWTTKNNKPLYSF EDNAGYVYDVMWSPTHPALFACVDGMGRLDL WNLNNDTEVPTASISVEGNPALNRVRWTHSGRE IAVGDSEGQIVIYDVGEQIAVPRNDEWARFGRTL AEINANRADAEEEAATRIPA

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3462	A	2	2643	TAPEFSRSTHASAHASVARVLRNREIAQLKKEQR RQEFQIRALESQKRQQEMVLRRKTQEVSALRRL AKPMSERVAGRAGLKPPMLDSGAEVSASTTSSE AESGARSVSSIVRQWNRKINHFLGDHPAPTVNGT RPARKKFQKKGASQSFSKAARLKWQSLERRIIDI VMQRMTIVNLEADMERLIKKREELFLLQEALRR KRERLQAESPEEEKGLQELAEEIEVLAANIDYIND GITDCQATIVQLEETKEELDSTDTSVVISSCSLAE ARLLLDNFLKASIDKGLQVAQKEAQIRLLEGRLR QTDMAGSSQNHLLLLDALREKAEAHPELQALIYN VQQENGYASTDEEISEFSEGSFSQSFTMKGSTSH DDFKFKSEPKLSAQMKAVSAECLGPPLDISTKNI TKSLASLVEIKEDGVGFSVRDPYYRDRVSRTVSL PTRGSTFPRQSRATETSPLTRRKSYDRGQPIRSTD VGFTPPSSPPTRPRNDRNVFSRLTSNQSQGSALD KSDDSDSSL\SEVLRGIISPVGGAKGARTAPLQCV SMAEGHTKPILCLDATDELLFTGSKDRSCKMWN LVTGQEIAALKGHPNNVVSIKYCSHSGLVFSVST SYIKVWDIRDSAKCIRTLTSSGQVISGDACAATST RAITSAQGEHQINQIALSPSGTMLYAASGNAVRI WELSRFQPVGKLTGHIGPVMCLTVTQTASQHDL VVTGSKDHYVKMFELGECVTGTIGPTHNFEPPH YDGIECLAIQGDILFSGSRDNGIKKWDLDQQELIQ QIPNAHKDWVCALAFIPGRPMLLSACRAGVIKV WNVDNFTPIGEIKGHDSPINAICTNAKHIFTASSG CRVKVWNYVPGLTPCLPRRVLAIKGRATTLP
3463	A	198	3146	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFA GVYRAESIHTGLEVAIKMIDKKAMYKAGMVQR VQNEVKIHCQLKHPSILELYNYFEDSNYVYLVLE MCHNGEMNRYLKNRVKPFSENEARHFMHQIITG MLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGL ATQLKMPHEKHYTLCGTPNYISPEIATRSAHGLE SDVWSLGCMFYTLLIGRPPFDTDTVKNTLNKVV LADYEMPTFLSIEAKDLIHQLLRRNPADRLSLSSV LDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAI TASSSTSISGSLFDKRRLLIGQPLPNKMTVFPKNK SSTDFSSSGDGNSFYTQWGNQETSNSGRGRVIQD AEERPHSRYLRRAYSSDRSGTSNSQSQAKTYTM ERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF NFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFP FADPTPQTETVQQWFGNLQINAHLRKTTEYDSIS PNRDFQGHPDLQKDTSKNAWTDTKVKKNSDAS DNAHSVKQQNTMKYMTALHSKPEIIQQECVFGS DPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHR LKPIRQKTKKAVVSILDSEEVCVELVKEYASQEY VKEVLQISSDGNTITIYYPNGG\RGFPLA\DRPPSP T\DNISR\YSF\DNLPEKYWRKYQYASRFVQLVRS KSPKITYFTRYAKCILMENSPGADFEVWFYDGV KIHKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIK MYMDHANEGHRICLALESIISEEERKTRSAPFFPII IGRKPGSTSSPKALSPPPSVDSNYPTRDRASFNRM VMHSAASPTQAPILNPSMVTNEGLGLTTTASGTD ISSNSLKDCLPKSAQLLKSVFVKNVGWATQ\LTS GAVWVQFNDGSQLVVQAGVSSISYTSPNGQ\TTR \YGENEKLPDYIKQKLQCLSSILLMFSNPTPNFH

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3464	A	14	348	AVRTVSGTSLGPRSHSRSPGRCHCFSAVTFSSPRL AASEAPDPMEEWDVPQMKKEVESLKYQLAFQR EMASKTIPELLKWIEDGIPKDPFLNPDLMKNNPW V\EKGKCTIL
3465	A	5537	405	VRKLDRERVGAWWRGAWARHPRQEAGEHAKR RKGHAETPRGRRKGRAGRSAAAVGELRPARRSL ETSRAAAAMAKDSPSPLGASPKKPGCSSPAAAV LENQRRELEKLRAELEAERAGWRAERRRFAARE RQLREEAERERRQLADRLRSKWEAQRSRELRQL QEEMQREREAEIRQLLRWKEAEQRQLQQLLHRE RDGVVRQARELQRQLAEELVNRGHCSRPGASEV SAAQCRCRLQEVLAQLRWQTDGEQAARIRYLQ AALEVERQLFLKYILAHFRGHPALSGSPDPQAVH SLEEPLPQTSSGSCHAPKPACQLGSLDSLSAEVG VRSRSLGLVSSACSSSPDGLLSTHASSLDCFAPAC SRSLDSTRSLPKASKSEERPSSPDTSTPGSRRLSPP PSPLPPPPPPSAHRKLSNPRGGEGSESQPCEVLTPS PPGLGHHELIKLNWLLAKALWVLARRCYTLQEE NKQLRRAGCPYQADEKVKRLKVKRAELTGLAR RLADRARELQETNLRAVSAPIPGESCAGLELCQV FARQRARDLSEQASAPLAKDKQIEELRQECHLLQ ARVASGPCSDLHTGRGGPCTQWLNVRDLDRLQ RESQREVLRLQRQLMLQQGNGGAWPEAGGQSA TCEEVRRQMLALERELDQRRRECQELGAQAAPA RRRGEEAETQLQAALLKNAWLAEENGRLQAKT DWVRKVEAENSEVRGHLGRACQERDASGLIAEQ LLQQAARGQDRQQQLQRDPQKALCDLHPSWKEI QALQCRPGHPPEQPWETSQMPESQVKGSRRPKF HARAEDYAVSQPNRDIQEKREASLEESPVALGES ASVPQVSETVPASQPLSKKTSSQSNSSSEGSMWA TVPSSPTLDRDTASEVDDLEPDSVSLALEMGGSA APAAPKLKIFMAQYNYNPFEGPNDHPEGELPLTA GDYTYIFGDMDEDGFYEGELEDGRRGLVPSNFVE QIPDSYIPGCLPAKSPDLGPSQLPAGQDEALEEDS LLSGKAQGVVDRGLCQMVRVGSKTEVATEILDT KTEACQLGLLQSMGKQGLSRPLLGTKGVLRMAP MQLHLQNVTATSANITWVYSSHRHPHVVYLDD REHALTPAGVSCYTFQGLCPGTHYRARVEVRLP RDLLQVYWGTMSSTVTFDTLLAGPPYPPLDVLV ERHASPGVLVVSWLPVTIDSAGSSNGVQVTGYA VYADGLKVCEVADATAGSTLLEFSQLQVPLTWQ KVSVRTMSLCGESLDSVPAQIPEDFFMCHRWPET PPFSYTCGDPSTYRVTFPVCPQKLSLAPPSAKASP HNPGSCGEPQAKFLEAFFEEPPRRQSPVSNLGSE GECPSSGAGSQAQELAEAWEGCRKDLLFQKSPQ NHRPPSVSDQTGEKENCYQHMGTSKSPAPGFIHL RTECGPRKEPCQEKAALERVLRQKQDAQGFTPP QLGASQQYASDFHNVLKEEQEALCLDLWGTERR EERREPEPHSRQGQALGVKRGCQLHEPSSALCPA PSAKVIKMPRGGPQQLGTGANTPARVFVALSDY NPLVMSANLKAAEEELVFQKRQLLRVWGSQDT HDFYLSECNRQVGNIPGRLVAEMEVGTEQTDRR WRSPAQGHLPSVAHLEDFQGLTIPQGSSLVLQGN SKRLPLWTPKIMIAALDYDPGDGQMGGQGKGRL ALRAGDVVMVY\GPMDDQGFYYGELGGHRG\L

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				VPANLRIKMSSQGH
3466	A	1	1111	MSKPPDLLLRLLRGAPRQRVCTLFIIGFKFTFFVSI MIYWHVVGEPKEKGQLYNLPAEIPCPTLTPPTPP SHGPTPGNIFFLETSDRTNPNFLFMCSVESAARTH PESHVLVLMKGLPGGNASLPRHLGISLLSCFPNV QMLPLDLRELFRDTPLADWYAAVQGRWEPYLL PVLSDASRIALMWKFGGIYLDTDFIVLKNLRNLT NVLGTQSRYVLNGAFLAFERRHEFMALCMRDFV DHYNGWIWGHQGPQLLTRVFKKWCSIRSLAESR ACRGVTTLPPEAFYPIPWQDWKKYFEDINPEELP RLLSATYAVHVWNKKSQGTRFEATSRALLAQLH ARYCPTTHE/DHENVLVKGPAGHLPNLLLMGHW
3467	A	1	2175	MAKVILKQSKQCKNLLTCKVAQVCPVCGCLHC YFWWLSGLESRRPSSPLIDIKPIEFGVLSAKKEPIQ PSVLRRTYNPDDYFRKFEPHLYSLDSNSDDVDSL TDEEILSKYQLGMLHFSTQYDLLHNHLTVRVIEA RDLPPPISHDGSRQDMAHSNPYVKICLLPDQKNS KQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLLL TVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHW WKAHDSQFSAPGLPADQQFFADLFSGLVLNPQL LGRVWFASQPASLPVGSLCIDFPRLDIVLRGEYG NLLEAKQQRLVEGEMLFIPARAANLPVNNKPVM LLSLVFAPTWLGLSFYDSRTTSLLHPARQIQLP\SL QRGEGEAMLS\ALTLFSRSPLEQNIIQPLVLSLLHL CGSVVNMPPGNSQPRGDFLYHSICTWVQDNYAQ PLTRESVAQFFNITPNHLSKLFAQHGTMRFIEYVR WVRMAKARMILQKYHLSIHEVAQRCGFPDSDYF CRVFRRQFGMDYVDILQIHRWDYNTPIEETLEAL NDVVKAGKARYIGASSMHASQFAQALELQKQH GWAQFVSMQDHYNLIYREEEREMLPLCYQEGV AVIPWSPLARGRLTRPWGETTARLVSDEVGKNL YKESDENDAQIAERLTGVSEELGATRAQVALAW LLSKPGIAAPIIGTSREEQLDELLNAVDITLKPEQI AELETPYKPHPVVGFK
3468	A	147	3209	ALPLPLPTLYPGMSRRKQRKPQQLISDCEGPSASE NGDASEEDHPQVCAKCCAQFTDPTEFLAHQNAC STDPPVMVIIGGQENPNNSSASSEPRPEGHNNPQ VMDTEHSNPPDSGSSVPTDPTWGPERRGEESSGH FLVAATGTAAGGGGGLILASPKLGATPLPPESTP APPPPPPPPPPPGVGSGHLNIPLILEELRVLQQRQI HQMQMTEQICRQVLLLGSLGQTVGAPASPSELP GTGTASSTKPLLPLFSPIKPVQTSKTLASSSSSSSS SSGAETPKQAFFHLYHPLGSQHPFSAGGVGRSHK PTPAPSPALPGSTDQLIASPHLAFPSTTGLLAAQC LGAARGLEATASPGLLKPKNGSGELSYGEVMGP LEKPGGRHKCRFCAKVFGSDSALQIHLRSHTGER PYKCNVCGNRFTTRGNLKVHFHRHREKYPHVQ MNPHPVPEHLDYVITSSGLPYGMSVPPEKAEEEA ATPGGGVERKPLVASTTALSATESLTLLSTSAGT ATAPGLPAFNKFVLMKAVEPKNKADENTPPGSE GSAISGVAESSTATRMQLSKLVTSLPSWALLTNH FKSTGSFPLPLCARALG\ASPSETSKLQQLVEKID RQGAVAVTSAASGAPTTSAPAPSSSASSGPNQCV ICLRVLSCPRALRLHYGQHGGERPFKCKVCGRAF STRGNLRAHFVGHKASPAARAQNSCPICQKKFT

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				NAVTLQQHVRMHLGGQIPNGGTALPEGGGAAQ ENGSEQSTVSGAGSFPQQQSQQPSPEEELSEEEEE EDEEEEEDVTDEDSLAGRGSESGGEKAISVRGDS EEASGAEEEVGTVAAAATAGKEMDSNEKTTQQS SLPPPPPPDSLDQPQPMEQGSSGVLGGKEEGGKP ERSSSPASALTPEGEATSVTLVEELSLQEAMRKEP GESSSRKACEVCGQAFPSQAAL\EEH\QKTHPKEG PLF\TCVFCRQGFLERATLKKHMLLAHHQVQPFA PHGPQNIAALSLVPGCSPSITSTGLSPFPRKDDPTI P
3469	A	3	5664	NLRPLSFALFLGDPNMANLEESFPRGGTRKIHKP EKAFQQSVEQDNLFDISTEEGSTKRKKSQKGPAK TKKLKIEKRESSKSAREKFEILSVESLCEGMRILG CVKEVNELELVISLPNGLQGFVQVTEICDAYTKK LNEQVTQEQPLKDLLHLPELFSPGMLVRCVVSSL GITDRGKKSVKLSLNPKNVNRVLSAEALKPGML LTGTVSSLEDHGYLVDIGVDGTRAFLPLLKAQEY IRQKNKGAKLKVGQYLNCIVEKVKGNGGVVSLS VGHSEVSTAIATEQQSWNLNNLLPGLVVKAQVQ KVTPFGLTLNFLTFFTGVVDFMHLDPKKAGTYFS NQAVRACILCVHPRTRVVHLSLRPIFLQPGRPLTR LSCQNLGAVLDDVPVQGFFKKAGATFRLKDGVL AYARLSHLSDSKNVFNPEAFKPGNTHKCRIIDYS QMDELALLSLRTSIIEAQYLRYHDIEPGAVVKGT VLTIKSYGMLVKVGEQMRGLVPPMHLADILMK NPEKKYHIGDEVKCRVLLCDPEAKKLMMTLKKT LIESKLPVITCYADAKPGLQTHGFIIRVKDYGCIV KFYNNVQGLVPKHELSTEYIPDPERVFYTGQVV KVVVLNCEPSKERMLLSFKLSSDPEPKKEPAGHS QKKGKAINIGQLVDVKVLEKTKDGLEVAVLPHN IRAFLPTSHLSDHVANGPLLHHWLQAGDILHRVL CLSQSEGRVLLCRKPALVSTVEGGQDPKNFSEIH PGMLLIGFVKSIKDYGVFIQLPSGLSGLAPKAIMS DKFVTSTSDHFVEGQTVAAKVTNVDEEKQRMLL SLRLSDCGLGDLAITSLLLLNQCLEELQGVRSLM SNRDSVLIQTLAEMTPGMFLDLVVQEVLEDGSV VFSGGPVPDLVLKASRYHRAGQEVESGQKKKVV ILNVDLLKLEVHVSLHQ\DLV\NRKARKLRKGSE HQAIVQHLEKSFAIASLVETGHLAAFSLTSHLND TFRFDSEKLQVGQGVSLTLKTTEPGVTGLLLAVE GPAAKRTMRPTQKDSETVDEDEEVDPALTVGTI KKHTLSIGDMVTGTVKSIKPTHVVVTLEDGIIGCI HASHILDDVPEGTSPTTKLKVGKTVTARVIGGRD MKTFKYLPISHPRFVRTIPELSVRPSELEDGHTAL NTHSVSPMEKIKQYQAGQTVTCFLKKYNVVKK WLEVEIAPDIRGRIPLLLTSLSFKVLKHPDKKFRV GQALRATVVGPDSSKTFLCLSLTGPHKLEEGEVA MGRVVKVTPNEGLTVSFPFGKIGTVSIFHMSDSY SETPLEDFVPQKVVRCYILSTADNVLTLSLRSSRT NPETKSKVEDPEINSIQDIKEGQLLRGYVGSIQPH GVFFRLGPSVVGLARYSHVSQHSPSKKALYNKH LPEGKLLTARVLRLNHQKNLVELSFLPGDTGKPD VLSASLEGQLTKQEERKTEAEERDQKGEKKNQK RNEKKNQKGQEEVEMPSKEKQQPQKPQAQKRG GRECRESGSEQERVSKKPKKAGLSEEDDSLVDV

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				YYREGKEEAEETNVLPKEKQTKPAEAPRLQLSSG FAWNVGLDSLTPALPPLAESSDSEEDEKPHQATI KKSKKERELEKQKAEKELSRTEEALMDPGRQPE SADDFDRLVLSSPNSSILWLQYMAFHLQATEIEK ARAVAERALKTISFREEQEKLNVWVALLNLENM YGSQESLTKVFERAVQYNEPLKVFLHLADIYAKS EKFQEAGELYNRMLKRFRQEKAVWIKYGAFLLR RSQAAASHRVLQRALECLPSKEHVDVIAKFAQL EFQLGDAERAKAIFENTLSTYPKRTDVWSVYID MTIKHGSQKDVRDIFERVIHLSLAPKRMKFFFKR YLDYEKQHGTEKDVQAVKAKALEYVEAKSSVL ED
3470	A	2334	1226	TAAAPVAPGTMDDATVLRKKGYIVGINLGKGSY AKVKSAYSERLKFNVAVKIIARKKTPTDFVERFL PREMDILATVNHGSIIKTYEIFETSDGRIYIIMELG VQGDLLEFIKCQGALHEDVARKMFRQLSSAVKY CHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKR CLRDSNGRIILSKTFCGSAAYAAPEVLQSIPYQPK VYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQK EHRVDFPRSKNLTCECKDLIYRMLQ\PDVS\KRLH IDEILSHSWLQPPKPK\ATSSASFKREGEGKYRAE CKLDTKTGLRPDHRPDHKLGAKTQHRLLVVPEN ENRMEDRLAETSRAKDHHISGAEVGKAST
3471	A	537	148	TERGAPQHPTLPLPSLTPSSVHTGQPKTTPSVILFL PSCEEPQANKATLVCLMNN/FYPGILMVTWKAD GTLITQSVEKTTPSKQSNNKYVASSYLSLTPEQW RSRRSYSCQVMQEGSTVEKSVAPAECS
3472	A	1	2272	DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQT WLPNHVVFLRLREGLKNQSPTEAEKPASSSLPSS PPPQLLTRNVVFGLGGELFLWDGEDSSFLVVRLR GPSGGGEEPALSQYQRLLCINPPLFEIYQVLLSPT QHHVALIGIKGLMVLELPKRWGKNSEFEGGKST VNCSTTPVAERFFTSSTSLTLKHAAWYPSEILDPH VVLLTSDNVIRIYSLREPQTPTNVIILSEAEEESLV LNKGRAYTASLGETAVAFDFGPLAAVPKTLFGQ NGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPN ILVIATESGMLYHCVVLEGEEEDDHTSEKSWDSR IDLIPSLYVFECVELELALKLASGEDDPFDSDFSC PVKLHRDPKCPSRYHCTHEAGVHSVGLTWIHKL HKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLP CRQPAPIRGFWIVPDILGPTMICITSTYECLIWPLL STVHPASPPLLCTREDVEVAESPLRVLAETPDSFE KHIRSILQRSVANPAFLKASEKDIAPPPEECLQLLS RATQVFREQYILKQDLAKEEIQRRVKLLCDQKK KQLEDLSYCREERKSLREMAERLADKYEEAKEK QEDIMNRMKKLLHSFHSELPVLSDSERDMKKEL QLIPDQLRHLGNAIKQVTMKKDYQQQKMEKVL SLPKPTIILSAYQRKCIQSILKEEGEHIREMVKQIN DIRNHVNF
3473	A	1	2272	DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQT WLPNHVVFLRLREGLKNQSPTEAEKPASSSLPSS PPPQLLTRNVVFGLGGELFLWDGEDSSFLVVRLR GPSGGGEEPALSQYQRLLCINPPLFEIYQVLLSPT QHHVALIGIKGLMVLELPKRWGKNSEFEGGKST

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				VNCSTTPVAERFFTSSTSLTLKHAAWYPSEILDPH VVLLTSDNVIRIYSLREPQTPTNVIILSEAEEESLV LNKGRAYTASLGETAVAFDFGPLAAVPKTLFGQ NGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPN ILVIATESGMLYHCVVLEGEEEDDHTSEKSWDSR IDLIPSLYVFECVELELALKLASGEDDPFDSDFSC PVKLHRDPKCPSRYHCTHEAGVHSVGLTWIHKL HKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLP CRQPAPIRGFWIVPDILGPTMICITSTYECLIWPLL STVHPASPPLLCTREDVEVAESPLRVLAETPDSFE KHIRSILQRSVANPAFLKASEKDIAPPPEECLQLLS RATQVFREQYILKQDLAKEEIQRRVKLLCDQKK KQLEDLSYCREERKSLREMAERLADKYEEAKEK QEDIMNRMKKLLHSFHSELPVLSDSERDMKKEL QLIPDQLRHLGNAIKQVTMKKDYQQQKMEKVL SLPKPTIILSAYQRKCIQSILKEEGEHIREMVKQIN DIRNHVNF
3474	A	4344	2550	DRRREPERHVRVKQRTSVLNMLRRLDKIRFRGH KRDDFLDLAESPNASDTECSDEIPLKVPRTSPRDS EELRDPAGPGTLIMATGVQDFNRTEFDRLNEIKG HLEIALLEKHFLQEELRKLREETNAEMLRQELDR ERQRRMELEQKVQEVLKARTEEQMAQQPPKGQ AQASNGAERRSQGLSSRLQKWFYERFGEYVEDF RFQPEENTVETEEPLSARRLTENMRRLKRGAKPV TNFVKNLSALSDWYSVYTSAIAFTVYMNAVWH GWAIPLFLFLAILRLSLNYLIARGWRIQWSIVPEV SEPVEPPKEDLTVSEKFQLVLDVAQKAQNLFGK MADILEKIKNLFMWVQPEITQKLYVALWAAFLA SCFFPYRLVGLAVGLYAGIKFFLIDFIFKRCPRLR AKYDTPYIIWRSLPTDPQLKERSSAAVSRRLQTTS SRSYVPSAPAGLGKEEDAGRFHSTKKGNFHEIFN LTENERPLAVCENGWRCCLINRDRKMPTDYIRN GVLYVT\ENYLCFESSKSGSSKRNKVIKLVDITDI QKYKVLSVLPGSGMGIAVSTPSTQKPLVFGAMV HRDEAFETILSQYIKITSAAASGGDS
3475	A	2	1126	TAARRRQKGAAAAAETHGQAKAKSGWLKPYYF IELMESRKDITNQEELWKMKPRRNLEEDDYLHK DTGETSMLKRPVLLHLHQTAHADEFDCPSELQH TQELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLA TSHQQYFYKIPILVINKVLPMVSITLLALVYLPGV IAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGL LSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQ VQQNKEDAL\IEHDVWRMEIYVSLGIVGLAILAL LAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIH ALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLI FKSILFLPCLRKKILKIRHGWEDVTKINKTEICSQL
3476	A	143	3191	AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRL DLILCNKTAYQEVFKPENISLRNKLRELCVKLMF LHPVDYGRKAEELLWRKVYYEVIQLIKTNKKHI HSRSTLECAYRTHLVAGIGFYQHLLLYIQSHYQL ELQCCIDWTHVTDPLIGCKKPVSASGKEMDWAQ MACHRCLVYLGDLSRYQNELAGVDTELLAERFY YQALSVAPQIGMPFNQLGTLAGSKYYNVEAMY CYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQL

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				KKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQ PKSSSVDSELTSLCQSVLEDFNLCLFYLPSSPNLS LASEDEEEYESGYAFLPDLLIFQMVIICLMCVHSL ERAGSKQYSAAIAFTLALFSHLVNHVNIRLQAEL EEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPP PVTPQVGEGRKSRKFSRLSCLRRRHPPKVGDDS DLSEGFESDSSHDSARASEGSDSGSDKSLEGGGT AFDAETDSEMNSQESRSDLEDMEEEEGTRSPTLE PPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQM FQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCV NGDVDKPSEPASEEGSESEGSESSGRSCRNERSIQ EKLQVLMAEGLLPAVKVFLDWLRTNPDLIIVCA QSSQSLWNRLSVLLNLLPAAGELQESGLALCPEV QDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAH RRFNFDTDRPLLSTLEESVVRICCIRSFGHFIARLQ GSILQFNPEVGIFVSIAQSEQESLLQQAQAQFRMA QEEARRNRLMRDMAQLRLQLEVSQLEGSLQQPK AQSAMSPYLVPDTQALCHHLPVIRQLATSGRFIVI IPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGN RYIRCQKEVGKSFERHKLKRQDADAWTLYKILD SCKQLTLAQGAGEEDPSGMVTIITGLPLDNPSVL SGPMQAALQAAAHASVDIKNVLDFYKQWKEIG
3477	A	1	3902	MTEPRERRGYSVPPRPEVGTQATEWRVEESNFN KIFLKKDAELGRSNHLPTWDKPEDASWLPQSCL GGDAVATTGEIHEEKAWKTRALEVGQPAQRDIR RGELWGKEHGADQAIQETLEDLSSLERTLVVSES SPLGGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQ ELGREERRRQAGAAFQVLQLPQALPIQVDSEEGL LSTGRRLDREQLCRQWDPCLVSFDVLATGDLALI HVEIQVLDINDHQPRFPKGEQELEISESASLRTRIP LDRALDPDTGPNTLHTYTLSPSEHFALDVIVGPD ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPP KSGTSLVKVNVLDSNDNSPAFAESSLALEIQEDA APGTLLIKLTATDPDQGPNGEVEFFLSKHMPPE\V LDTFSIDAKTGQVILRRPLDYEKNPAYEVDVQAR DLGPNPIPAHCKVLIKVLDVNDNIPSIHVTWASQP SLVSEALPKDSFIALVMADDLDSGNNGLVHCWL SQELGHFRLKRTNGNTYMLLTNATLDREQWPK YTLTLLAQDQGLQPLSAKKQLSIQISDINDNAPVF EKSRYEVSTRENNLPSLHLITIKAHDADLGINGK VSYRIQDSPVAHLVAIDSNTGEVTAQRSLNYEEM AGFEFQVIAEDSGQPMLASSVSVWVSLLDANDN APEVVQPVLSDGKASLSVLVNASTGHLLVPIETP NGLGPAGTDTPPLATHSSRPFLLTTIVARDADSG ANGEPLYSIRSGNEAHLFILNPHTGQLFVNVTNA SSLIGSEWELEIVVEDQGSPPLQTRALLRVMFVTS VDHLRDSARKPGALSMSMLTVICLAVLLGIFGLI LALFMSICRTEKKDNRAYNCREAESTYRQQPKR PQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDV DKEAMMEAGWDPCLQAPFHLTPTLYRTLRNQG NQGAPAESREVLQDTVNLLFNHPRQRNASRENL NLPEPQPATGQPRSRPLKVAGSPTGRLAGDQGSE EAPQRPPASSATLRRQRHLNGKVSPEKESGPRQI LRSLVRLSVAAFAERNPVEELTVDSPPVQQISQLL SLLHQGQFQPKPNHRGNKYLAKPGGSRSAIPDTD

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				GPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEE LSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTN YRDNVISPDAAATEEPRTFQTFGKAEAPELSPTG TRLASTFVSEMSSLLEMLLEQRSSMPVEAASEAL RRLSVCGRTLSLDLATSAASGMKVQGDPGGKTG TEGKSRGSSSSSRCL
3478	A	13	1620	TLPPPGNSGCHRLCFPEFEFLQVTKMEFSGRKWR KLRLAGDQRNASYPHCLQFYLQPPSENISLIEFEN LAIDRVKLLKSVENLGVSYVKGTEQYQSKLESEL RKLKFSYRENLEDEYEPRRRDHISHFILRLAYCQS EELRRWFIQQEMDLLRFRFSILPKDKIQDFLKDSQ LQFEAISDEEKTLREQEIVASSPSLSGLKLGFESIY KIPFADALDLFRGRKVYLEDGFAYVPLKDIVAIIL NEFRAKLSKALALTARSLPAVQSDERLQPLLNHL SHSYTGQDYSTQGNVGKISLDQIDLLSTKSFPPC MRQLHKALRENHHLRHGGRMQYGLFLKGIGLT LEQALQFWKQEFIKGKMDPDKFDKGYSYNIRHS FGKEGKRTDYTPFSCLKIILSNPPSQGDYHGCPFR HSDPELLKQKLQSYKISPGGISQILDLVKGTHYQ V\ACQKYFEMIHTVDDCGFS\LSHPNQYFCESQRI LNGGKDIKKEPIQPETPQPKPSVQKTKDASSALA SLNSSLEMDMEGLEDYFSEDS
3479	A	698	138	RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVR AQPLSVTVWAPRCQRP/QPPAPEPSSPNAAVPEAI PTPRAAASAALELPLGPAPVSVAPQAEAEARSTP GPAGSRLGPETFRQRFRQFRYQDAAGPREAFRQL REL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILP EAARARRIRRRTDVRITG
3480	A	117	2226	RRGSRSRGPFAEPAAPGGLCSSSEEKTEEGGMAV GLCKAMSQGLVTFRDVALDFSQEEWEWLKPSQ KDLYRDVMLENYRNLVWLGLSISKPNMISLLEQ GKEPWMVERKMSQGHCADWESWWEIEELSPK WFIDEDEISQEMVMERLASHGLECSSFREAWKY KGEFELHQGNAERHFMQVTAVKEISTGKRDNEF SN/IWEKHTPEISIFNTTES\PTIQQVHKFDIYDKLF PQNSVIIEYKRLHAEKESLIGNECEEFNQSTYLSK DIGIPPGEKPYESHDFSKLLSFHSLFTQHQTTHFG KLPHGYDECGDAFSCYSFFTQPQRIHSGEKPYAC NDCGKAFSHDFFLSEHQRTHIGEKPYECKECNKA FRQSAHLAQHQRIHTGEKPFACNECGKAFSRYAF LVEHQRIHTGEKPYECKECNKAFRQSAHLNQHQ RIHTGEKPYECNQCGKAFSRRIALTLHQRIHTGE KPFKCSECGKTFGYRSHLNQHQRIHTGEKPYECI KCGKFFRTDSQLNRHHRIHTGERPFECSKCGKAF SDALVLIHHKRSHAGEKPYECNKCGKAFSCGSY LNQHQRIHTGEKPYECSECGKAFHQILSLRLHQRI HAGEKPYKCNESQRVRRSELAVSRGLTTKPADT GPDSTLNAAKVAEPARAGTEAALRPALSVAESA TSLGPLHQGRRFPEAPAAHPGGTGFTVCAS
3481	A	2	1522	ASRHGMTPGALLMLLGALGPPLAPGVRGSEAEG RLREKLFSGYDSSVRPAREVGDRVRVSVGLILAQ LISLNEKDEEMSTKVYLDLEWTDYRLSWDPAEH DGIDSLRITAESVWLPDVVLLNNNDGNFDVALDI SVVVSSDGSVRWQPPGIYRSSCSIQVTYFPFDWQ NCTMVFSSYSYDSSEVSLQTGLGPDGQGHQEIHI

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				HEGTFIENGQWENIHKPSRLIQPPGDPRGGREGQ RQEVIFYLIIRRKPLFYLVNVIAPCILITLLAIFVFY LPPDAGEKMGLSIFALLTLTVFLLLLADKVPETSL SVPIIIKYLMFTMVLVTFSVILSVVVLNLHHRSPH THQMPLWVRQIFIHKLPLYLRLKRPKPERDLMPE PPHCSSPGSGWGRGTDEYFIRKPPSDFLFPKPNRF QPELSAPDLRRFIDGPNRAVALLPELREVVSSISYI ARQLQEQEDHDALKEDWQFVAMVVDRLFLWTF IIFTSVGTL\VIFLDATYHLPPPDPFP
3482	A	1273	172	ERWDSGGADAEWYALADWTAVWLPRSDFYTR LQTGEGHVPALRLPAGMPPDSPRELVPKQAPCSP SDPALPWTLGHGNQPPAVVPEPQGPMGPAGVAA RPGRFFGVYLLYCLNPRYRVR\VYVGFTVNTARR VQQHNGGRKKGGA\GRTSGRGPWEMVLVVHGF PSSVAALRFEWAWQHPHASRRLAHVGPRLRGET AFAFHLRVLAHMLRAPPWARLPLTLRWVRPDLR QDLCLPPPPHVLLAFGPPPAQVPRPQRRRAGPFD DAEPEPDQGDPGACCSLCAQTIQDEEGPLCCPHP GCLLRAHVICLAEEFLQEEPGQLLPLEGQCPCCE KSLLWGDLIWLCQMDTEKEVEDSELEEAHWTD LLET
3483	A	230	3686	WRPWPCIDTSWNLQVAARTLRVSSAQCGLVPT MARVESPVPAARASLTGSCVLGQAMPLRGGAGP SPASHGPTHGPSDPRTCLPGRGAGGMRPHGRGA LGCCGLCSFYTCHGAAGDEIMHQDIVPLCAADIQ DQLKKRFAYLSGGRGQDGSPVITFPDYPAFSEIPD KEFQNVMTYLTSIPSLQDAGIGFILVIDRRRDKW TSVKASVLRIAASFPANLQLVLVLRPTGFFQRTLS DIAFKFNRDDFKMKVPVIMLSSVPDLHGYIDKSQ LTEDLGGTLDYCHSRWLCQRTAIESFALMVKQT AQMLQSFGTELAETELPNDVQST\SSVLCAHTEK KDKAKEDLRLALKEGHSVLESLRELQAEGSEPSV NQDQLDNQATVQRLLAQLNETEAAFDEFWAKH QQKLEQCLQLRHFEQGFREVKAILDAASQKIATF TDIGNSLAHVEHLLRDLANFQEKSGVFVERARA LSLTASSFIGNKHYAVDSIRPKCQELRHLCDQFSA EIARRRGLLSKSLELHRRLETSMKWCDEGIYLLA SQPVDKCQSQDGAEAALQEIEKFLETGAENKIQE LNAIYKEYESILNQDLMEHVRKVFQKQASMEEV FHRRQASLKKLAARQTRPVQPVAPRPEALAKSP CPSPGIRRGSENSSSEGGALRRGPYRRAKSEMSES RQGRGSAGEEEESLAILRRHVMSELLDTERAYVE ELLCVLEGYAAEMDNPLMAHLLSTGLHNKKDV LFGNMEEIYHFHNRIFLRELENYTDCPELVGRCF LERMEDFQIYEKYCQNKPRSESLWRQCSDCPFFQ ECQRKLDHKLSLDSYLLKPVQRITKYQLLLKEM LKYSRNCEGAEDLQEALSSILGILKAVNDSMHLI AITGYDGNLGDLGKLLMQGSFSVWTDHKRGHT KVKELARFKPMQRHLFLHEKAVLFCKKREENGE GYEKAPSYSYKQSLNMAAVGITENVKGDAKKFE IWYNAREEVYIVQAPTPEIKAAWVNEIRKVLTSQ LQACREASQHRALEQSQSLPLPAPTSTSPSRGNSR NIKKLEERKTDPLSLEGYVSSAPLTKPPEKGKGW SKTSHSLEAPEDDGGWSSAEEQINSSDAEEDGGL GPKKLVPGKYTVVADHEKGGPDALRVRSGDVV

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				ELVQEGDEGLW
3484	A	208	6103	VTMAQQAADKYLYVDKNFINNPLAQADWAAK KLVWVPSDKSGFEPASLKEEVGEEAIVELVENGK KVKVNKDDIQKMNPPKFSKVEDMAELTCLNEAS VLHNLKERYYSGLIYTYSGLFCVVINPYKNLPIYS EEIVEMYKGKKRHEMPPHIYAITDTAYRSMMQD REDQSILCTGESGAGKTENTKKVIQYLAYVASSH KSKKDQGELERQLLQANPILEAFGNAKTVKNDN SSRFGKFIRINFDVNGYIVGANIETYLLEKSRAIRQ AKEERTFHIFYYLLSGAGEHLKTDLLLEPYNKYR FLSNGHVTIPGQQDKDMFQETMEAMRIMGIPEEE QMGLLRVISGVLQLGNIVFKKERNTDQASMPDN TAAQKVSHLLGINVTDFTRGILTPRIKVGRDYVQ KAQTKEQADFAIEALAKATYERMFRWLVLRINK ALDKTKRQGASFIGILDIAGFEIFDLNSFEQLCINY TNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFG LDLQPCIDLIEKPAGPPGILALLDEECWFPKATDK SFVEKVMQEQGTHPKFQKPKQLKDKADFCIIHY AGKVDYKADEWLMKNMDPLNDNIATLLHQSSD KFVSELWKDVDRIIGLDQVAGMSETALPGAFKT RKGMFRTVGQLYKEQLAKLMATLRNTNPNFVR CIIPNHEKKAGKLDPHLVLDQLRCNGVLEGIRICR QGFPNRVVFQEFRQRYEILTPNSIPKGFMDGKQA CVLMIKALELDSNLYRIGQSKVFFRAGVLAHLEE ERDLKITDVIIGFQACCRGYLARKAFAKRQQQLT AMKVLQRNCAAYLKLRNWQWWRLFTKVKPLL QVSRQEEEMMAKEEELVKVREKQLAAENRLTE METLQSQLMAEKLQLQEQLQAETELCAEAEELR ARLTAK\KQ\ELEEICHDLEARVEEEEERCQHLQA EKKKMQQNIQELEEQLEEEESARQKLQLEKVTT EAKLKKLEEEQIILEDQNCKLAKEKKLLEDRIAEF TTNLTEEEEKSKSLAKLKNKHEAMITDLEERLRR EEKQRQELEKTRRKLEGDSTDLSDQIAELQAQ\IA ELKMQLAKKEEELQAALARVEEEAAQKNMALK KIRELESQISELQEDLKCER\ASRNKAEKQKRDLG EELEALKTELEDTLDSTAAQQELRSKREQEVNIL KKTLEEEAKTHEAQIQEMRQKHSQAVEELAEQL EQTKRVKANLEKAKQTLENERGELANEVKVLLQ GKGDSEHKRKKVEAQLQELQVKFNEGERVRTEL ADKVTKLQVELDNVTGLLSQSDSKSSKLTKDFS ALESQLQDTQELLQEENRQKLSLSTKLKQVEDE KNS\FREQLEEEEEAKHNLEKQIATLHAQVADM KKKMEDSVGCLETAEEVKRKLQKDLEGLSQRHE EKVAAYDKLEKTKTRLQQELDDLLVDLDHQRQ SACNLEKKQKKFDQLLAEEKTISAKYAEERDRA EAEAREKETKALSLARALEEAMEQKAELERLNK QFRTEMEDLMSSKDDVGKSVHELEKSKRAIEQQ VEEMKTQLEELEDELQATEDAKLRLEVNLQAM KAQFERDLQGRDEQSEEKKKQLVRQVREMEAE LEDERKQRSMAVAARKKLEMDLKDLEAHIDSA NKNRDEAIKQLRKLQAQMKDCMRELDDTRASR EEILAQAKENEKKLKSMEAEMIQLQEELAAAER AKRQAQQERDELADEIANSSGKGALALEEKRRL EARIAQLEEELEEEQGNTELINDRLKKANLQIDQI NTDLNLERSHAQKNENARQQLERQNKELKVKL

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				QEMEGTVKSKYKASITALEAKIAQLEEQLDNETK ERQAACKQVRRTEKKLKDVLLQVDDERRNAEQ YKDQADKASTRLKQLKRQLEEAEEEAQRANASR RKLQRELEDATETADAMNREVSSLKNKLRRGDL PFVVPRRMARKGAGDGSDEEVDGKADGAEAKP AE
3485	A	2	1782	CSTGVSKAPLTYLMSYGFELGWRKGNRAVACR EDRGGESVGMGQESILSQVHWWEAEPVEKTPGR DSEATIMSLRVHTLPTLLGAVVRPGCRELLCLLM ITVTVGPGASGVCPTACICATDIVSCTNKNLSKVP GNLFRLIKRLDLSYNRIGLLDSEWIPVSFAKLNTL ILRHNNITSISTGSFSTTPNLKCLDLSSNKLKT\VK NAVFQELKVLEVLLLYNNHISYLDPSAFGGLSQL QKLYLSGNFLTQFPMDLYVGRFKLAELMFLDVS YNRIPSMPMHHINLVPGKQLRGIYLHGNPFVCD\ CSLVSLLVFWYRRHFSSVMDFKNDYTCRLWSDS RHSRQVLLLQDSFMNCSDSIINGSFRALGFIHEAQ VGERLMVHCDSKTGNANTDFIWVGPDNRLLEPD KEMENFYVFHNGSLVIESPRFEDAGVYSCIAMNK QRLLNETVDVTINVSNFTVSRSHAHEAFNTAFTT LAACVASIVLVLLYLYLTPCPCKCKTKRQKNML HQSNAHSSILSPGPASDASADERKAGAGKRVVFL EPLKDTAAGQNGKVRLFPSEAVIAEGILKSTRGK SDSDSVNSVFSDTPFVAST
3486	A	357	1173	GDPRETKVFPSRSFARNTVGVSHHQSHLFHTVSR IYVEDKHKILYCEVPKAGCSNWKRILMVLNGLA SSAYNISHNAVHYGKHLKKLDSFDLKGIYTRLDT YTK\LVLVRDPMERLVSAFRDKFDHPNSYYHPVF GKAIIKKYRPNACEEALINGSGVKFKEFIHYLLDS HRPVGMDIHWEKVSKLCYPCLINYDFVGKFETL EEDANYFLQMIGAPKELKFPNFKDRHSSDERTNA QVVRQYLKDLTRTERQLIYDFYYLDYLMFNYTT PFL
3487	A	2	3281	CDKSGAVPFSTTRSPRRPSPRSAGPSLSSVSPRSQ LWASSGLSEEHAAPLLPAWPRHPCPPSLTPGPSM AQGAMRFCSEGDCAISPPRCPRRWLPEGPVPQSP PASMYGSTGSLLRRVAGPGPRGRELGRVTAPCTP LRGPPSPRVAPSPWAPSSPTGQPPPGAQSSVVIFR FVEKASVRPLNGLPAPGGLSRSWDLGGVSPPRPT PALGPGSNRKLRLEASTSDPLPARGGSALPGSRN LVHGPPAPPQVGADGLYSSLPNGLGDPPERLATL FGGPADTGFLNQGDTWSSPREVSSHAQRIARAK WEFFYGSLDPPSSGAKPPEQAPPSPPGVGSRQGS GVAVGRAAKYSETDLDTVPLRCYRETDIDEVLA EREEADSAIESQPSSEGPPGTAYPPAPRPGPLPGP HPSLGSGNEDEDDDEAGGEEDVDDEVFEASEGA RPGSRMPLKSPVPFLPGTSPSADGPDSFSCVFEAI LESHRAKGTSYTSLASLEALASPGPTQSPFFTFEL PPQPPAPRPDPPAPAPLAPLEPDSGTSSAADGPWT QRGEEEEAEARAKLAPGREPPSPCHSEDSLGLGA APLGSEPPLSQLVSDSDSELDSTERLALGSTDTLS NGQKADLEAAQRLAKRLYRLDGFRKADVARHL GKNNDFSKLVAGEYLKFFVFTGMTLDQALRVFL KELALMGETQERERVLAHFSQRYFQCNPEALSSE DGAHTLTCALMLLNTDLHGHNIGKRMTCGDFIG

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				NLEGLNDGGDFPRELLKALYSSIKNEKLQWAIDE EELRRFLSELADPNPKVIKRISGGSGSGSSPFLDLT PEPGAAVYKHGALVRKVHADPDCRKTPRGKRG WKSFHGILKGMILYLQKEEYKPGKALSETELKN AISIHHALATRAS\NYSKRPHVFYLRTADWRVFL FQAPSLEQMQSWITRINVVAAMFSAPPFPAAVSS QKKFSRPLLPSAATRLSQEEQVRTHEAKLKAMA SELREHRAAQLGKKGRGKEAEEQRQKEAYLEFE KSRYSTYAALLRVKLKAGSEELDAVEAALAQAG STEDGLPPSHSSPSLQPKPSSQPRAQRHSSEPRPG AGSGRRKP
3488	A	441	1968	GTETPHCWGRGTAGLRRELDREERDGPGTATMS FPHFGHPYRGAFQFL\ASASSSTTCCESTLRSVSY VASGSTPAPALCCAP\YDSRLLGSARPELGAALGI YGAPYAAAAAAQSYPGYLPYSPEPPSLYGALNP QYEFKEAAGSFTSSLAQPGAYYPYERTLGQYQY ERYGAVELSGAGRRKNATRETTSTLKAWLNEHR KNPYPTKGEKIMLAIITKMTLTQVSTWFANARRR LKKENKMTWAPKNKGGEERKAEGGEEDSLGCL TADTKEVTASQEARGLRLSDLEDLEEEEEEEEA EDEEVVATAGDRLTEFRKGAQSLPGPCAAAREG RLERRECGLAAPRFSFNDPSGSEEADFLSAETGSP RLTMHYPCLEKPRIWSLAHTATASAVEGAPPARP RPRSPECRMIPGQPPASARRLSVPRDSACDESSCI PKAFGNPKFALQGLPLNCAPCPRRSEPVVQCQYP SGAEGSGPPAALGVSMQKTPTYRPARQLHTLCH SSLP
3489	A	718	2073	IAAYHKALSYRGHVHANNRGTNNVHFTPPPSPS RGILPMNPRNMMNHSQVGQGIGIPSRTNSMSSSG LGSPNRSSPSIICMPKQQPSRQPFTVNSMSGFGMN RNQAFGMNNSLSSNIFNGTDGSENVTGLDLSDFP ALADRNRREGSGNPTPLINPLAGRAPYVGMVTK PANEQSQDFSIHNEDFPALPGSSYKDPTSSNDDSK SNLNTSGKTTSSTDGPKFPGDKSSTTQNNNQQKK GIQVLPDGRVTNIPQGMVTDQFGMIGLLTFIRAA ETDPGMVHLALGSDLTTLGLNLNSPENLYPKFAS PWASSPCRPQDIDFHVPSEYLTNIHIRDKLFFFFS W/TAIKLGRYGEDLLFYLYYMNGGDVLQLLAAV ELFNRDWRYHKEERVWITRAPGMEPTMKTNTY ERGTYYFFDCLNWRKVAKEFHLEYDKLEERPHL PSTFNYNPAQQAF
3490	A	2	2833	FVAKMATSQYFDFAQGGGPQYSTQAPTLPLPTV GASYTGQPTPGMDPAVNPAFPPAAPAGYGGYQP HSGQDFAYGSRPQEPVPTATTMATYQDSYSYGQ SAAARSYEDRPYFQSAALQSGRMTAADSGQPGT QEACGQPSPHGSHSHAQPPQQAPIVESGQPASTL SSGYTYPTATGVQPESSASIVTSYPPPSYNPTCTA YTAPSYPNYDASVYSAASPFYPPAQPPPPPGPPQ QLPPPPAPAGSGSSPRADSKPPLPSKLPRPKAGPR QLQLHYCDICKISCAGPQTYREHLGGQKHRKKE AAQKTGVQPNGSPRGVQAQLHCDLCAVSCTGA DAYAAHIRGSKHQKVFKLHAKLGKPIPTLEPALA TESPPGAEAKPTSPTGPSVCASSRPALAKRPVASK ALCEGPPEPQAAGCRPQWGKPAQPKLEGPGAPT QGGSKEAPAGCSDAQPVGPEYVEEVFSDEGRVL

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				RFHCKLCECSFNDLNAKDLHVRGRRHRLQYRKK VNPDLPIATEPSSRARKVLEERMRKQRHLAEERL EQLRRWHAERRRLEEEPPQDVPPHAPPDWAQPL LMGRPESPASAPLQPGRRPASSDDRHVMCKHATI YPTEQELLAVQRAVSHAERALKLVSDTLAEEDR GRREEEGDKRSSVAPQTRVLKGVMRVGILAKGL LLRGDRNVRLALLCSEKPTHSLLRRIAQQLPRQL QMVTEDEYEVSSDPEANIVISSCEEPRMQVTISVT SPLMREDPSTDPGVEEPQADAGDVLSPKKCLESL AALRHARWFQARASGLQPCVIVIRVLRDLCRRV PT\WGALPAWAMELLVEKAVSSAAGPLGPGDAV RRVLECVATGTLLTDGPGLQDPCERDQTDALEP MTLQEREDVTASAQHALRMLAFRQTHKVLGMD LLPPRHRLGARFRKRQRGPGEGEEGAGEKKRGR RGGEGLV
3491	A	2	1321	FVGDGALSGCRRGRAPRVPSMAGSLPPCVVDCG TGYTKLGYAGNTEPQFIIPSCIAIRESAKVVDQAQ RRVLRGVDDLDFFIGDEAIDKPTYATKWPIRHGII EDWDLMERFMEQVVFKYLRAEPEDHYFLMTEP PLNTPENREYLAEIMFESFNVPGLYIAVQAVLAL AASWTSRQVGERTLTGIVIDSGDGVTHVIPVAEG YVIGSCIKHIPIAGRDITYFIQQLLREREVGIPPEQS LETAKAIKEKYCYICPDIVKEFAKYDVDPRKWIK QYTGINAINQKKFVIDVGYERFLGPEIFFHPEFAN PDFMESISDVVDEVIQNCPIDVRRPLYKNVVLSG GSTMFRDFGRRLQRDLKRVVDARLRLSEELSGG\ RIKPKPVEVQVVTHHMQRYAV\WFGG\SMLASTP EFFQVCHTKKDYEEYGPSICRHNPVFGVMS
3492	A	3	2024	PNGVALLHLPGAAVIPNTNYMFQDALGGRSRGS REESPAPSRAPASASLWRRLVVVEAKMAAHAAA AAQAAAAQAAHAEAADSWYLALLGFAEHFRTS SPPKIRLCVHCLQAVFPFKPPQRIEARTHLQLGSV LYHHTKNSEQARSHLEKAWLISQQIPQFEDVKFE AASLLSELYCQENSVDAAKPLLRKAIQISQQTPY WHCRLLFQLAQLHTLEKDLVSACDLLGVGAEY ARVVGSEYTRALFLLSKGMLLLMERKLQEVHPL LTLCGQIVENWQGNPIQKESLRVFFLVLQVTHYL DAGQVKSVKPCLKQLQQCIQTISTLHDDEILPSNP ADLFHWLPKEHMCVLVYLVTVMHSMQAGYLE KAQKYTDKALMQLEKLKMLDCSPILSSFQVILLE HIIMCRLVTGHKATALQEISQVCQLCQQSPRLFS NHAAQLHTLLGLYCVSVNCMDNAEAQFTTALR LTNHQELWAFIVTNLASVYIREGNRHQEVV\LYS LLERINPDHSFPVSSHCLRAAAFYVRGLFSFFQGR YNEAKRFLRETLKMSNAEDLNRLTACSLVLLGHI FYVLGNHRESNNMVVPAMQLASKIPDMSVQLW SSALLRDLNKACGNAMDAHEAAQMHQNFSQQL LQDHIEACSLPEHNLITWTDGPPPVQFQAQNGPN TSLASLL
3493	A	3	2024	PNGVALLHLPGAAVIPNTNYMFQDALGGRSRGS REESPAPSRAPASASLWRRLVVVEAKMAAHAAA AAQAAAAQAAHAEAADSWYLALLGFAEHFRTS SPPKIRLCVHCLQAVFPFKPPQRIEARTHLQLGSV LYHHTKNSEQARSHLEKAWLISQQIPQFEDVKFE AASLLSELYCQENSVDAAKPLLRKAIQISQQTPY

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				WHCRLLFQLAQLHTLEKDLVSACDLLGVGAEY ARVVGSEYTRALFLLSKGMLLLMERKLQEVHPL LTLCGQIVENWQGNPIQKESLRVFFLVLQVTHYL DAGQVKSVKPCLKQLQQCIQTISTLHDDEILPSNP ADLFHWLPKEHMCVLVYLVTVMHSMQAGYLE KAQKYTDKALMQLEKLKMLDCSPILSSFQVILLE HIIMCRLVTGHKATALQEISQVCQLCQQSPRLFS NHAAQLHTLLGLYCVSVNCMDNAEAQFTTALR LTNHQELWAFIVTNLASVYIREGNRHQEVV\LYS LLERINPDHSFPVSSHCLRAAAFYVRGLFSFFQGR YNEAKRFLRETLKMSNAEDLNRLTACSLVLLGHI FYVLGNHRESNNMVVPAMQLASKIPDMSVQLW SSALLRDLNKACGNAMDAHEAAQMHQNFSQQL LQDHIEACSLPEHNLITWTDGPPPVQFQAQNGPN TSLASLL
3494	A	2	1615	VLRGQRGPAGGLAEERRRGRNEWRIHDVTTAPF PGLVQRRSRLLIVSQVRYFLKNKVSPDLCNEDGL TALHQCCIDNFEEIVKLLLSHGANVNAKDNELW TPLHAAATCGHINLVKILVQYGADLLAVNSDGN MPYDLCEDEPTLDVIETCMAYQGITQEKINEMRV APEQQMIADIHCMIAAGQDLDWIDAQGATLLHI AGANGYLRAAELLLDHGVRVDVKDWDGWEPL HAAAFWGQMQMAELLVSHGAN\LNARTSMDE MPIDLCEEEEFKVLLLELK\HKHDVIMKSQLRHK SSLSRRTSHRQAS/SVGKVVRRTQPVGTGPNL\YR KEYE/GEEAILWQRSA\AEDQRTSTYNGDIRET\R TDQENKDPNPRLEK\PVLLSEFPTKIPRGELDMPV ENGLRAPVSAYQYALANGDVWKVHEVPDYSM AYGNPGVADATPPWSSYKEQSPQTLLELKRQRA AAKLLSHPFLSTHLGSSMARTGESSSEGKAPLIG GRTSPYSSNGTSVYYTVTSGDPPLLKFKAPIEEM EEKVHGCCRIS
3495	A	327	1078	APMADTTPNGPQGAGAVQFMMTNKLDTAMWL SRLFTVYCSALFVLPLLGLHEAASFYQRALLANA LTSALRLHQRLPHFQLSRAFLAQALLEDSCHYLL YSLIFVNSYPVTMSIFPVLLFSLLHAATYTKKVL\ DARG\SNSLPLLR\SVLDKLSANQQNILKFIACNEI FLMPATVFMLFSGQGSLLQPFIYYRFLTLRYSSRR NPYCRTLFNELRIVVEHIIMKPACPLFVRRLCLQS IAFISRLAPTVP
3496	A	3	2867	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAP APGTPAASGWQPPTYHSGRAFSARYPRPSRRGYS SHHGPSWRKKYSLVNRPPGPSDPPADHAVRPLH GARGGQPPVPQQHVLERQVQLSQGQNVVIKVKP PSKSGSASASGAQRGSLEEFEDTPWSDQRPREGE GEPPRGQLQPSRPTRARGTCSVEDPLLVCQKEPG KPRMVKSVGSVGDSPREPRRTVSESVIAVKASFP SSALPPRTGVALGRKLGSHSVASCAPQLLGDRRV DAGHTDQPVPSGSVGGPARPASGPRQAREASLV VTCRTNKFRKNNYKWVAASSKSPRVARRALSPR VAAENVCKASAGMANKVEKPQLIADPEPKPRKP ATSSKPGSAPSKYKWKASSPSASSSSSFRWQSEA GSKDHASQLSPVLSRSPSGD\RPALAHSGLKPLSG ETPLSAYKVKTRTKIIRRRGSTSLPGDKKSGTSPA ATAKSHLSLRRRQALRGKSSPVLKKTPNKGLVQ

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				VTKHRLCRLPPSRAHLPTKEASSLHAVRTAPTSK VIKTRYRIVKKTPASPLSAPPFPLSLPSWRARRLS LSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYR CIGGVLYKVSANKLSKTSGQPSDAGSRPLLRTGR LDPAGSCSRSLASRAVQRSLAIIRQARQRREKRK EYCMYYNRFGRCNRGERCPYIHDPEKVAVCTRF VRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGI CSNSNCPYSHVYVSRKAEVCSDFLKGYCPLGAK CKKKHTLLCPDFARRGACPRGAQCQLLHRTQKR HSRRAATSPAPGPSDATARSRVSASHGPRKPSAS QRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSS KASSSSSSSSSPPASLDHE\APSLQEAALAAACSN RLCKLPSFISLQSSPSPGAQPRVRAPRAPLTKDSG KPLHIKPRL
3497	A	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCR NLQEFLGGLSPGVLDRLYGHPATCLAVFRELPSL AKNWVMRMLFLEQPLPQAAVALWVKKEFSKA QEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQN LRIALLGGGKAWSDDTSQLGPDKHARDVPSLDK YAEERWEVVLHFMVGSPSAAVSQDLAQLLSQA GLMKSTEPGEPPCITSAGFQFLLLDTPAQLWYFM LQYLQTAQSRGMDLVEILSFLFQLSFSTLGKDYS VEGMSDSLLNFLQHLREFGLVFQRKRKSRRYYP T/RALAINLSSGVSGAGGTVHQPGFIV\VETNYRL YAYTESELQIALIALFSEMLYPFP\NMVV\ARVTR\ ESVQQAIASGITAQQIIHFLRTRAHPVMLKQTPVL PPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF ELL\LAHAPKLGVLVFE/NTPAKRLMVVTPAGHS DVKRFWKRQKHSS
3498	A	790	190	RDLGPAALMTASASSFSSSQGVQQPSIYSFSQITR SLFLSNGVAANDKLLLSSNRITAIVNASVGSGQRI LRG\LQYIKVPVTDARDSRLYDFFDPIADLIHTVS MRQGRTLLNCMAG\MSRSASLCLAYLMKYHSM S\LLDAHTWA/TKSRRPIIRPNNGFWEQLINYEFK LFNNNTVRMINSPVGNIPDIYEKDLRMMISM
3499	A	31	1586	TAGFLLAPLEMQRLLTPVKRILQLTRAVQETSLT PARLLPVAHQRFSTASAVPLAKTDTWPKDVGIL ALEVYFPAQYVDQTDLEKYNNVEAGKYTVGLG QTRMGFCSVQEDINSLCLTVVQRLMERIQLPWD SVGRLEVGTETIIDKSKAVKTVLMELFQDSGNTD IEGIDTTNACYGGTASLFNAANWMESSSWDGRY AMVVCGDIAVYPSGNARPTGGAGAVAMLIGPK APLALERGLRGTHMENVYDFYKPNLASEYPIVD GKLSIQCYLRALDRCYTSYRKKIQNQWKQAGSD RPFTLDDLQYMIFHTPFCKMVQKSLARLMFNDF LSASSDTQTSLYKGLEAFGGLKLEDTYTNKDLD KALLKASQDMFDKKTKASLYLSTHNGNMYTSSL YGCLASLLSHHSAQELAGSRIGAFSYGSGLAASF FSFRVSQDAAPGSPL\DKLVSSTSDLPKRLASRKC VSPEEFTEIMNQREQFYHKVNFSPPGDTNSLFPGT WYLERVDEQHRRKYARRPV
3500	A	185	2692	MLPTEVPQSHPGPSALLLLQLLLPPTSAFFPNIWS LLAAPGSITHQDLTEEAALNVTLQLFLEQPPPGRP PLRLEDFLGRTLLADDLFAAYFGPGSSRRFRAAL GEVSRANAAQDFLPTSRNDPDLHFDAERLGQGR

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				ARLVGALRETVVAARALDHTLARQRLGAALHA LQDFYSHSNWVELGEQQPHPHLLWPRQELQNLA QVADPTCSDCEELSCPRNWLGFTLLTSGYFGTHP PKPPGKCSHGGHFDRSSSQPPRGGINKDSTSPGFS PHHMLHLQAAKLALLASIQAFSLLRSRLGDRDFS RLLDITPASSLSFVLDTTGSMGEEINAAKIQARHL VEQRRGSPMEPVHYVLVPFHDPGFGPVFTTSDPD SFWQQLNEIHALGGGDEPEMCLSALQLALLHTPP LSDIFVFTDASPKDAFLTNQVESLTQERRCRVTFL VTEDTSRVQGRARREILSPLRFEPYKAVALASGG EVIFTKDQHIRDVAAIVGESMAALVTLPLDPPVV VPGQPLVFSVDGLLQKITVRIHGDISSFWIKNPAG VSQGQEEGGGPLGHTRRFGQFWMVTMDDPPQT GTWEIQVTAEDTPGVRVQAQTSLDFLFHFGIPME DGPHPGLYPLTQPVAGLQTQLLVEVTGLGSRAN PGDPQPHFSHVILRGVPEGAELGQVPLEPVGPPE RGLLAASLSPTLLSTPRPFSLELIGQDAAGRRLHR AAPQPSTVVPVLLELSGPSGFLAPGSKVPLSLRIA SFSGPQDLDLRTFVNPSFSLTSNLSRAHLELNESA WGRLWLEVPDSAAPDSVVMVTVTAGGREANPV PPTHAFLRLLVSAPAPQDRH
3501	A	1245	5815	RRAHPSHSRLSPYLSVSRDPYFFVTVSRTILTLSA PAPPRRTPAPSMGTALLQRGGCFLLCLSLLLLGC WAELGSGLEFPGAEGQWTRFPKWNACCESEMSF QLKTRSARGLVLYFDDEGFCDFLELILTRGGRLQ LSFSIFCAEPATLLADTPVNDGAWHSVRIRRQFR NTTLFIDQVEAKWVEVKSKRRDMTVFSGLFVGG LPPELRAAALKLTLASVREREPFKGWIRDVRVNS SQVLPVDSGEVKLDDEPPNSGGG\SPCEAGEEGE GGVCLNGGVCSVVDDQAVCDCSRTGFRGKDCS QEDNNVEGLAHLMMGDQGKEEYIATFKGSEYF CYDLSQNPIQSSSDEITLSFKTLQRNGLMLHTGKS ADYVNLALKNGAVSLVINLGSGAFEALVEPVNG KFNDNAWHDVKVTRNLRQHSGIGHAMVTISVD GILTTTGYTQEDYTMLGSDDFFYVGGSPSTADLP GSPVSNNFMGCLKEVVYKNNDVRLELSRLAKQ GDPKMKIHGVVAFKCENVATLDPITFETPESFISL PKWNAKKTGSISFDFRTTEPNGLILFSHGKPRHQ KDAKHPQMIKVDFFAIEMLDGHLYLLLDMGSGT IKIKALLKKVNDGEWYHVDFQRDGRSGTISVNT LRTPYTAPGESEILDLDDELYLGGLPENKAGLVF PTEVWTALLNYGYVGCIRDLFIDGQSKDIRQMA EVQSTAGVKPSCSKETAKPCLSNPCKNNGMCRD GWNRYVCDCSGTGYLGRSCEREATVLSYDGSM FMKIQLPVVMHTEAEDVSLRFRSQRAYGILMAT TSRDSADTLRLELDAGRVKLTVNLDCIRINCNSS KGPETLFAGYNLNDNEWHTVRVVRRGKSLKLT VDDQQAMTGQMAGDHTRLEFHNIETGIITERRY LSSVPSNFIGHLQSLTFNGMAYIDLCKNGDIDYC ELNARFGFRNIIADPVTFKTKSSYVALATLQAYT SMHLFFQFKTTSLDGLILYNSGDGNDFIVVELVK GYLHYVFDLGNGANLIKGSSNKPLNDNQWHNV MISRDTSNLHTVKIDTKITTQITAGARNLDLKSDL YIGGVAKETYKSLPKLVHAKEGFQGCLASVDLN G\RLP\DLISDGSFSCNGTDSRRGMWKGPSTT\CQ

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				EDSCSNQGVCLQQWDGFSCDCSMTSFSGPLCND PGTTYIFSKGGGQITYKWPPNDRPSTRADRLAIGF STVQKEAVLVRVDSSSGLGDYLELHIHQGKIGVK FNVGTDDIAIEESNAIINDGKYHVVRFTRSGGNA TLQVDSWPVIERYPAGRQLTIFNSQATIIIGGKEQ GQPFQGQLSGLYYNGLKVLNMAAENDANIAIVG NVRLVGEVPSSMTTESTATAMQSEMSTSIMETTT TLATSTARRGKPPTKEPISQTTDDILVASAECPSD DEDIDPCEPSSGGLANPTRAGGREPYPGSAEVIRE SSSTTGMVVGIVAAAALCILILLYAMYKYRNRDE GSYHVDESRNYISNSAQSNGAVVKEKQPSSAKSS NKNKKNKDKEYYV
3502	A	394	72	KPAHLPFTVIIMPKRKPSEGAMSDKVKA/KFELQ RRSAGLFSKPTPPKPETRPKKDPANQRQKLPKVR KGKADA/SKEGNSPAEERCSMVQTQKVEGWRSG SELPVALSF
3503	A	43	3358	SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRPLS SLPPPPSRALAPTRAPDTALTIMEVAEVESPLNPS CKIMTFRPSMEEFREFNKYLAYMESKGAHRAGL AKVIPPKEWKPRQCYDDIDNLLIPAPIQQMVTGQ SGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRY LDYEDLERKYWKNLTFVAPIYGADINGSIYDEGV DEWNIARLNTVLDVVEEECGISIEGVNTPYLYFG MWKTTFAWHTEDMDLYSINYLHFGEPKSWYAIP PEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLIS PSVLKKYGIPFDKITQEAGEFMITFPYGYHAGFN HGFNCAESTNFATVRWIDYGKVAKLCTCRKDM VKISMDIFVRKFQPDRYQLWKQGKDIYTIDHTKP TPASTPEVKAWLQRRRKVRKASRSFQCARSTSK RPKADEEEEVSDEVDGAEVPNPDSVTDDLKVSE KSEAAVKLRNTEASSEEESSASRMQVEQNLSDHI KLSGNSCLSTSVTEDIKTEDDKAYAYRSVPSISSE ADDSIPLSTGYEKPEKSDPSELSWPKSPESCSSVA ESNGVLTEGEEESDVESHGNGLEPGEIPAVPSGER NSFKVPSIAEGENKTSKSWRHPLSRPPARSPMTL VKQQAPSDEELPEVLSIEEEVEETESWAKPLIHL WQTKPPNFAAEQEYNATVARMKPHCAICTLLMP YHKPDSSNEENDARWETKLDEVVTSEGKTKPLIP EMCFIYSEENIEYSPPNAFLEEDGTSLLISCAKCC VRVHASCYGIPSHEICDGWLCARCKRNAWTAEC CLCNLRGGALKQTKNNKWAHVMCAVAVPEVR FTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVS GACIQCSYGRCPASFHVTCAHAAGVL\MEPDDW PYVVNITCFRHKVNPNVKSKACEKVISVGQTVIT KHRNTRYYSCRVMAVTSQTFYEVMFDDGSFSRD TFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLY GAKYFGSNIAHMYQVEFEDGSQIAMKREDIYTL DEELPKRVKARFVSAGRCHLGTCQVNSLSSPHVS QAQQETYLGFWINSKKSQCNIFLSGTY
3504	A	1124	139	RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHR SRAWTCYLAIRMLMATCCPSPTTTACTGPWQRA PPLRLLVQKREADSSGLAFASNSLQRRKKGLLLR PVAPLRTRPPLLISLPQDFRQVSSVIDVDLLPETH RRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LER VPGIFISRLVRGGLAESTGLLAVSDEILEVNGIEV

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				AGKTLNQVTDMMVANSHN\LIVTVKPANQRNN VVRGASGRLTGPPSAGPGPAEPDSDDDSSDLVIE NRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPS LDDQEQASSGWGSRIRGDGSGFSL
3505	A	3	2898	SCRSATSQSGCGGGRSWLCSSLKMAAQPPRGIRL SALCPKFLHTNSTSHTWPFSAVAELIDNAYDPDV NAKQIWIDKTVINDHICLTFTDNGNGMTSDKLH KMLSFGFSDKVTMNGHVPVGLYGNGFKSGSM\R LGKDAIVFTKNGESMSVGLLSQTYL\EVIKAEHV VVPIVAFNKHRQMINLAESKASLAAILEHSLFSTE QKLLAELDAIIGKKGTRIIIWNLRSYKNATEFDFE KDKYDIRIPEDLDEITGKKGYKKQERMDQIAPES DYSLRAYCSILYLKPRMQIILRGQKVKTQLVSKS LAYIERDVYRPKFLSKTVRITFGFNCRNKDHYGI MMYHRNRLIKAYEKVGCQLRANNMGVGVVGII ECNFLKPTHNKQDFDYTNEYRLTITALGEKLND YWNEMKVKKNTEYPLNLPVEDIQKRPDQTWVQ CDACLKWRKLPDGMDQLPEKWYCSNNP\DPQFR NCEVPEEPEDEDLVHPTYEKTYKKTNKEKFRIRQ PEMIPRINAELLFRPT\ALSTPS\FSSPKESVSKR/RH LSEGTNSYATRLLNNHQVPPQSEPESNSLKRRLS TRSSILNAKNRRL\SSQF\ENSVYKG\DDDDEDVII LEENSTPKPAVDHDIDMKSEQSHVEQGGVQVEF VGDSEPCGQTGSTSTSSSRCDQGNTAATQTEVPS LVVKKEETVEDEIDVRNDAVILPSCVEAEAKIHE TQETTDKSADDAGCQLQELRNQLLLVTEEKENY KRQCHMFTDQIKVLQQRILEMNDKYVKKETCH QSTETDAVFLLESINGKSESPDHMVSQYQQALEE IERLKKQCSALQHVKAECSQCSNNESKSEMDEM AVQLDDVFRQLDKCSIERDQYKSEVELLEMEKS QIRSQCEELKTEVEQLKSTNQQTATDVSTSSNIEE SVNHMDGESLKLRSLRVNVGQLLAMIVPDLDLQ QVNYDVDVVDEILGQVVEQMSEISST
3506	A	2	2120	RPPEAGGRYRAGGRRQAAKPSRPPLPSRRRLPQG GRTRRAMDRPAAAAAAGCEGGGGPNPGPAGGR RPPRAAGGATAGSRQPSVETLDSPTGSHVEWCK QLIAATISSQISGSVTSENVSRDYKALRDGNKLA QMEEAPLFPGESIKAIVKDVMYICPFMGAVSGTL TVTDFKLYFKNVERDPHFILDVPLGVISRVEKIGA QSHGDNSCGIEIVCKDMRNLRLAYK\QEEQSKLG IFENLNKHAFPLSNGQALFAFSYKEKFPINGWKV YDPVSEYKRQGLPNESWKISKINSNYEFCDTYPA IIVVPTSVKDDDLSKVAVFLAKGRVPVLSWIHPE SQATITRCSQPLVGPNDKRCKEDEKYLQTIMDAN AQSHKLIIFDARQNSVADTNKTKGGGYESESAYP NAELVFLEIHNIHVMRESLRKLKEIVYPSIDEARW LSNVDGTHWLEYIRMLLAGAVRIADKIESGKTSV VVHCSDGWDRTAQLTSLAMLMLDSYYRTIKGFE TLVEKEWISFGHRFALRVGHGNDNHADADRSPIF LQFVDCVWQMTRQFPSAFEFNELFLITILDHLYS CLFGTFLCNCEQQRFKEDVYTKTISLWSYINSQL DEFSNPFFVNYENHVLYPVASLSHLELWVNYYV RWNPRMRPQMPIHQNLKELLAVRAELQKRVEG LQREVATRAVSSSSERGSSPSHFATSVHTLV
3507	A	1	2169	GSSIKIRLTVLCAKNLAKKDFFRLPDPF\AKIVVD

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				GSGQCHSTDTVKNTLDPKWNQHYDLYVGKTDSI TISVWNHKKIHKKQGAGFLGCVRLLSNAISRLKD TGYQRLDLCKLNPSDTDAVRGQIVVSLQTRDRIG TGGSVVDCRGLLENEGTVYEDSGPGRPLSCFME EPAPYTDSTGAAAGGGNCRFVESPSQDQRLQAQ RLRNPDVRGSLQTPQNRPHGHQSPELPEGYEQRT TVQGQVYFLHTQTGVSTWHDPRIPRDLNSVNCD ELGPLPPGWEVRSTVSGRIYFVDHNNRTTQFTDP RLHHIMNHQCQLKEPSQPLPLPSEGSLEDEELPA QRYERDLVQKLKVLRHELSLQQPQAGHCRIEVS REEIFEESYRQIMKMRPKDLKKRLMVKFRGEEG LDYGGVAREWLYLLCHEMLNPYYGLFQYSTDNI YMLQINPDSSINPDHLSYFHFVGRIMGLAVFHGH YINGGFTVPFYKQLLGKPIQLSDLESVDPELHKSL VWILENDITPVLDHTFCVEHNAFGRILQHELKPN G\RNVPVTEENKKEYVRLYVNWRFMRGIEAQFL ALQKGFNELIPQHLLKPFDQKELELIIGGLDKIDL NDWKSNTRLKHCVADSNIVRWFWQAVETFDEE RRARLLQFVTGSTRVPLQGFKALQGSTG\AAGPR LFTIHLIDANTDNLRKAHTCFNRIDIPPYESYEKL YEKLLTAVEETCGFAVE
3508	A	3	6388	ILYINPADLGWNPPVSSWIEKREIQTERANLTILF DKYLPTCLDTLRTRFKKIIPIPEQSMVQMVCHLLE CLLTTEDIPADCPKEIYEHYFVFAAIWAFGGAMV QDQLVDYRAEFSKWWLTEFKTVKFPSQGTIFDY YIDPETKKFEPWSKLVPQFEFDPEMPLQACLVHT SETIRVCYFMERLMARQRPVMLVGTAGTGKSVL VGAKLASLDPEAYLVKNVPFNYYTTSAMLQAVL EKPLEKKAGRNYGPPGNKKLIYFIDDMNMPEVD AYGTVQPHTIIRQHLDYGHWYDRSKLSLKEITNV QYVSCMNPTAGSFTINPRLQRHFSVFVLSFPGAD ALSSIYSIILTQHLKLGNFPASLQKSIPPLIDLALAF HQKIATTFLPTGIKFHYIFNLRDFANIFQGILFSSV ECVKSTWDLIRLYLHESNRVYRDKMVEEKDFDL FDKIQTEVLKKTFDDIEDPVEQTQSPNLYCHFAN GIGEPKYMPVQSWELLTQTLVEALENHNEVNTV MDLVLFEDAMRHVCHINRILESPRGNALLVGVG GSGKQSLTRLAAFISSMDVFQITLRKGYQIQDFK MDLASLCLKAGVKNLNTVFLMTDAQVADERFL VLINDLLASGEIPDLYSDDEVENIISNVRNEVKSQ GLVDNRENCWKFFIDRIRRQLKVTLCFSPVGNKL RVRSRKFPAIVNCTAIHWFHEWPQQALESVSLRF LQNTEGIEPTVKQSISKFMAFVHTSVNQTSQSYLS NEQRYNYTTPKSFLEFIRLYQSLLHRHRKELKCK TERLENGLLKLHSTSAQVDDLKAKLAAQEVELK QKNEDADKLIQVVGVETDKVSREKAMADEEEQ KVAVIMLEVKQKQKDCEEDLAKAEPALTAAQA ALNTLNKTNLTELKSFGSPPLAVSNVSAAVMVL MAPRGRVPKDRSWKAAKVTMAKVDGFLDSLIN FNKENIHENCLKAIRPYLQDPEFNPEFVATKSYA AAGLCSWVINIVRFYEVFCDVEPKRQALNKATA DLTAAQEKLAAIKAKIAHLNENLAKLTARFEKA TADKLKCQQEAEVTAVTISLANRLVGGLASENV RWADAVQNFKQQERTLCGDILLITAFISYLGFFT KKYRQSLLDRTWRPYLSQLKTPIPVTPALDPLRM

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				LMDDADVAAWQNEGLPADRMSVENATILINCE RWPLMVDPQLQGIKWIKNKYGEDLRVTQIGQKG YLQIIEQALEAGAVVLIENLEESIDPVLGPLLGRE VIKKGRFIKIGDKECEYNPKFRLILHTKLANPHYQ PELQAQATLINFTVTRDGLEDQLLAAVVSMERP DLEQLKSDLTKQQNGFKITLKTLEDSLLSRLSSAS GNFLGETVLVENLEITKQTAAEVEKKVQEAKVT EVKINEAREHYRPAAARASLLYFIMNDLSKIHPM YQFSLKAFSIVFQKAVERAAPDESLRERVANLID SITFSVYQYTIRGLFECDKLTYLAQLTFQILLMNR EVNAVELDFLLRSPVQTGTASPVEFLSHQAWGA VKVLSSMEEFSNLDRDIEGSAKSWKKFVESECPE KEKLPQEWKNKTALQRLCMLRAMRPDRMTYAL RDFVEEKLGSKYVVGRALDFATSFEESGPATPMF FILSPGVDPLKDVESQGRKLGYTFNNQNFHNVSL GQGQEVVAEAALDLAAKKGHWVILQNTLEMCS RETEFKSILFALCYFHAVVAERRKFGPQGWNRSY PFNTGDLTISVNVLYNFLEANAKVPYDDLRYLFG EIMYGGHITDDWDRRLCRTYLGEFIRPEMLEGEL SLAPGFPLPGNMDYNGYHQYIDAELPPESPYLYG LHPNAEIGFLTQTSEKLFRTVLELQPRDSQARDG AGATREEKVKALLEEILERVTDEFNIPELMAKVE ERTPYIVVAFQECGRMNILTREIQRSLRELELGLK GELTMTSHMENLQNALYFDMVPESWARRAYPS TAGLAAWFPDLLNRIKELEAWTGDFTMPSTVWL TGFFNPQSFLTAIMQSTARKNEWPLDQMALQCD MTKKNREEFRSPPREGAYIHGLFMEGACWDTQA GIITEAKLKDLTPPMPVMFIKAIPAD\RQDCGHVY SCPVTKTSQ\RDPTYVWTFNLKTKENPSKWVLA GVALLLQI
3509	A	3	6388	ILYINPADLGWNPPVSSWIEKREIQTERANLTILF DKYLPTCLDTLRTRFKKIIPIPEQSMVQMVCHLLE CLLTTEDIPADCPKEIYEHYFVFAAIWAFGGAMV QDQLVDYRAEFSKWWLTEFKTVKFPSQGTIFDY YIDPETKKFEPWSKLVPQFEFDPEMPLQACLVHT SETIRVCYFMERLMARQRPVMLVGTAGTGKSVL VGAKLASLDPEAYLVKNVPFNYYTTSAMLQAVL EKPLEKKAGRNYGPPGNKKLIYFIDDMNMPEVD AYGTVQPHTIIRQHLDYGHWYDRSKLSLKEITNV QYVSCMNPTAGSFTINPRLQRHFSVFVLSFPGAD ALSSIYSIILTQHLKLGNFPASLQKSIPPLIDLALAF HQKIATTFLPTGIKFHYIFNLRDFANIFQGILFSSV ECVKSTWDLIRLYLHESNRVYRDKMVEEKDFDL FDKIQTEVLKKTFDDIEDPVEQTQSPNLYCHFAN GIGEPKYMPVQSWELLTQTLVEALENHNEVNTV MDLVLFEDAMRHVCHINRILESPRGNALLVGVG GSGKQSLTRLAAFISSMDVFQITLRKGYQIQDFK MDLASLCLKAGVKNLNTVFLMTDAQVADERFL VLINDLLASGEIPDLYSDDEVENIISNVRNEVKSQ GLVDNRENCWKFFIDRIRRQLKVTLCFSPVGNKL RVRSRKFPAIVNCTAIHWFHEWPQQALESVSLRF LQNTEGIEPTVKQSISKFMAFVHTSVNQTSQSYLS NEQRYNYTTPKSFLEFIRLYQSLLHRHRKELKCK TERLENGLLKLHSTSAQVDDLKAKLAAQEVELK QKNEDADKLIQVVGVETDKVSREKAMADEEEQ

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				KVAVIMLEVKQKQKDCEEDLAKAEPALTAAQA ALNTLNKTNLTELKSFGSPPLAVSNVSAAVMVL MAPRGRVPKDRSWKAAKVTMAKVDGFLDSLIN FNKENIHENCLKAIRPYLQDPEFNPEFVATKSYA AAGLCSWVINIVRFYEVFCDVEPKRQALNKATA DLTAAQEKLAAIKAKIAHLNENLAKLTARFEKA TADKLKCQQEAEVTAVTISLANRLVGGLASENV RWADAVQNFKQQERTLCGDILLITAFISYLGFFT KKYRQSLLDRTWRPYLSQLKTPIPVTPALDPLRM LMDDADVAAWQNEGLPADRMSVENATILINCE RWPLMVDPQLQGIKWIKNKYGEDLRVTQIGQKG YLQIIEQALEAGAVVLIENLEESIDPVLGPLLGRE VIKKGRFIKIGDKECEYNPKFRLILHTKLANPHYQ PELQAQATLINFTVTRDGLEDQLLAAVVSMERP DLEQLKSDLTKQQNGFKITLKTLEDSLLSRLSSAS GNFLGETVLVENLEITKQTAAEVEKKVQEAKVT EVKINEAREHYRPAAARASLLYFIMNDLSKIHPM YQFSLKAFSIVFQKAVERAAPDESLRERVANLID SITFSVYQYTIRGLFECDKLTYLAQLTFQILLMNR EVNAVELDFLLRSPVQTGTASPVEFLSHQAWGA VKVLSSMEEFSNLDRDIEGSAKSWKKFVESECPE KEKLPQEWKNKTALQRLCMLRAMRPDRMTYAL RDFVEEKLGSKYVVGRALDFATSFEESGPATPMF FILSPGVDPLKDVESQGRKLGYTFNNQNFHNVSL GQGQEVVAEAALDLAAKKGHWVILQNTLEMCS RETEFKSILFALCYFHAVVAERRKFGPQGWNRSY PFNTGDLTISVNVLYNFLEANAKVPYDDLRYLFG EIMYGGHITDDWDRRLCRTYLGEFIRPEMLEGEL SLAPGFPLPGNMDYNGYHQYIDAELPPESPYLYG LHPNAEIGFLTQTSEKLFRTVLELQPRDSQARDG AGATREEKVKALLEEILERVTDEFNIPELMAKVE ERTPYIVVAFQECGRMNILTREIQRSLRELELGLK GELTMTSHMENLQNALYFDMVPESWARRAYPS TAGLAAWFPDLLNRIKELEAWTGDFTMPSTVWL TGFFNPQSFLTAIMQSTARKNEWPLDQMALQCD MTKKNREEFRSPPREGAYIHGLFMEGACWDTQA GIITEAKLKDLTPPMPVMFIKAIPAD\RQDCGHVY SCPVTKTSQ\RDPTYVWTFNLKTKENPSKWVLA GVALLLQI
3510	A	390	3330	AAGSGSRPPAPAARKMADLAECNIKVMCRFRPL NESEVNRGDKYIAKFQGEDTVVIASKPYAFDRVF QSSTSQEQVYNDCAKKIVKDVLEGYNGTIFAYG QTSSGKTHTMEGKLHDPEGMGIIPRIVQDIFNYIY SMDENLEFHIKVSYFEIYLDKIRDLLDVSKTNLSV HEDKNRVPYVKGCTERFVCSPDEVMDTIDEGKS NRHVAVTNMNEHSSRSHSIFLINVKQENTQTEQK LSGKLYLVDLAGSEKVSKTGAEGAVLDEAKNIN KSLSALGNVISALAEGSTYVPYRDSKMTRILQDS LGGNCRTTIVICCSPSSYNESETKSTLLFGQRAKTI KNTVCVNVELTAEQWKKKYEKEKEKNKILRNTI QWLENELNRWRNGETVPIDEQFDKEKANLEAFT VDKDITLTNDKPATAIGVIGNFTDAERRKCEEEIA KLYKQLDDKDEEINQQSQLVEKLKTQMLDQEEL LASTRRDQDNMQAELNRLQAENDASKEEVKEV LQALEELAVNYDQKSQEVEDKTKEYELLSDELN

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				QKSATLASIDAELQKLKEMTNHQKKRAAEMMA SLLKDLAEIGIAVGNNDVKQPEGTGMIDEEFTVA RLYISKMKSEVKTMVKRCKQLESTQTESNKKME ENEKELAACQLRISQHEAKIKSLTEYLQNVEQKK RQLEESVDALSEELVQLRAQEKVHEMEKEHLNK VQTANEVKQAVEQQIQSHRETHQKQISSLRDEVE AKAKLITDLQDQNQKMMLEQERLRVEHEKLKA TDQEKSRKLHELTVMQDRREQARQDLKGLEETV AKELQTLHNLRKLFVQDLATRVKKSAEIDS\DDT GGSAAQKQKISFLENNLE\QLTKSAQTSWYRDNA DLRCELPKLEKRLRATAERVKALESALKEAKEN ASRDRKRYQQEVDRIKEAVRSKNMARRGHSAQI AKPIRPGQHPAASPTHPSAIRGGGAFVQNSQPVA VRGGGGKQV
3511	A	1	1757	MASVQASRRQWCYLCDLPKMPWAMVWDFSEA VCRGCVNFEGADRIELLIDAARQLKRSHVLPEGR SPGPPALKHPATKDLAAAAAQGPQLPPPQAQPQP SGTGGGVSGQDRYDRATSSGRLPLPSPALEYTLG SRLANGLGREEAVAEGARRALLGSMPGLMPPGL LAAAVSGLGSRGLTLAPGLSPARPLFGSDFEKEK QQRNADCLAELNEAMRGRAEEWHGRPKAVREQ LLALSACAPFNVRFKKDHGLVGRVFAFDATARP PGYEFELKLFTEYPCGSGNVYAGVLAVARQMFH DALREPGKALASSGFKYLEYERRHGSGEWRQLG ELLTDGVRSFREPAPAEALPQQYPEPAPAALCGP PPRAPSRNLAPTPRRRKASPEPEGEAAGKMTTEE QQQRHWVAPGGPYSAETPGVPSPIAALKNVAEA LGHSPKDPGGGGGPVRAGGASPAASSTAQPPTQ HRLVARNGEAEVSPTAGAEAVSGGGSGTGATPG APLC\CTLCRERLEDTHFVQ\CPPVPEHKFCFPCSR KFIKAQGPAGE\VYCPSGDKCPLVGSSVPWAFMQ GEIATILAGDIKVKKERDP
3512	A	3	1994	NTNSSSVTNSAAGVEDLNIVQVTVPDNEKERLSS IEKIKQLREQVNDLFSRKFGEAIGVDFPVKVPYR KITFNPGCVVIDGMPPGVVFKAPGYLEISSMRRIL EAAEFIKFTVIRPLPGLELSNGEYSTVGKRKIDQE GRVFQEKWERAYFFVEVQNISTCLICKRSMSVSK EYNLRRHYQTNHSKHYDQYMERMRDEKLHELK KGLRKYLLGLSDTECPEQKQVFANPSPTQKSPVQ PVEDLAGNLWEKLREKIRSFVAYSIAIDEITDINN TTQLAIFIRGVDENFDVSEELLDTVPMTGTKSGN EIFSRVEKSLKNFCINWSKLVSVASTGTPPMVDA NNGLVTKLKSRVATFCKGAELKSICCIIHPESLCA Q\KLKMDHVMDVVVKSVNWICSRGLNHSEFTTL LYELDSQYGSLLYYTEIKWLSRGLVLKRFFESLE EIDSFMSSRGKPLPQLSSIDWIRDLAFLVDMTMH LNALNISLQGHSQIVTQMYDLIRAFLAKLCLWET HLTRNNLAHFPTLKLVSRNESDGLNYIPKIAELK TEFQKRLSDFKLYESELTLFSSPFSTKIDSVHEELQ MEVIDLQCNTVLKTKYDKVGIPEFYKYLWGSYP KYKHHCAKILSMFGSTYICEQLFSIMKLSKTKYC SQLKDSQWDSVLHIAT
3513	A	1836	513	FKSLLSVKWFCFSILVLIFLGTRCYWEMTQSRPSP DPHRGRWEGGRSRPKGGEEGRRRTRVPGLVTAS GPGNPLPDRLGEMAGGRHRRVVGTLHLLLLLVAA

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				LPWASRGVSPSASAWPEEKNYHQPAILNSSALRQ IAEGTSISEMWQNDLQPLLIERYPGSPGSYAARQ HIMQRIQRLQADWVLEIDTFLSQTPYGYRSFSNII STLNPTAKRHLVLACHYDSKYFSHW\NNRVFVG ATDSAVPCAMMLELARALDKKLLSLKTVSDSKP DLSLQLIFFDGEEAFLHWSPQDSLYGSRHLAAKM ASTPHPPGARGTSQLHGMDLLVLLDLIGAPNPTF PNFFPNSARWFERLQAIEHELHELGLLKDHSLEG RYFQNYSYGGVIQDDHIPFLRRGVPVLHLIPSPFP EVWHTMDDNEENLDESTIDNLNKILQVFVLEYL HL
3514	A	1836	513	FKSLLSVKWFCFSILVLIFLGTRCYWEMTQSRPSP DPHRGRWEGGRSRPKGGEEGRRRTRVPGLVTAS GPGNPLPDRLGEMAGGRHRRVVGTLHLLLLVAA LPWASRGVSPSASAWPEEKNYHQPAILNSSALRQ IAEGTSISEMWQNDLQPLLIERYPGSPGSYAARQ HIMQRIQRLQADWVLEIDTFLSQTPYGYRSFSNII STLNPTAKRHLVLACHYDSKYFSHW\NNRVFVG ATDSAVPCAMMLELARALDKKLLSLKTVSDSKP DLSLQLIFFDGEEAFLHWSPQDSLYGSRHLAAKM ASTPHPPGARGTSQLHGMDLLVLLDLIGAPNPTF PNFFPNSARWFERLQAIEHELHELGLLKDHSLEG RYFQNYSYGGVIQDDHIPFLRRGVPVLHLIPSPFP EVWHTMDDNEENLDESTIDNLNKILQVFVLEYL HL
3515	A	114	754	LCRDLTTTMSSKRTKTKTKKRPQRATSNVFAMF DQSQIQEFKEAFNMIDQNRDGFIDKEDLHDMLAS LGKNPTDEYLDAMMNEAPGPINFTMFLTMFGEK LNGTDPEDVIRNAFACFDEEATGTIQEDYLRELL TT\MGDRF\TDE\EVDELYREAPI\DKKGGIFNYI\E FTRHLETGGPKDKDDRKITFQIPSPNVPWLATFG VFLEIFLLHGP
3516	A	1	5169	MAAAPSALLLLPPFPVLSTYRLQSRSRPSAPETDD SRVGGIMRGEKNYYFRGAAGDHGSCPTTTSPLA SALLMPSEAVSSSWSESGGGLSGGDEEDTRLLQL LRTARDPSEAFQALQAALPRRGGRLGFPRRKEAL YRALGRVLVEGGSDEKRLCLQLLSDVLRGQGEA GQLEEAFSLALLPQLVVSLREENPALRKDALQIL HICLKRSPGEVLRTLIQQGLESTDARLRASTALLL PILLTTEDLLLGLDLTEVIISLARKLGDQETEEESE TAFSALQQIGERLGQDRFQSYISRLPSALRRHYN RRLESQFGSQVPYYLELEASGFPEDPLPCAVTLS NSNLKFGIIPQELHSRLLDQEDYKNRTQAVEELK QVLGKFNPSSTPHSSLVGFISLLYNLLDDSNFKVV HGTLEVLHLLVIRLGEQVQQFLGPVIAASVKVLA DNKLVIKQEYMKIFLKLMKEVGPQQVLCLLLEH LKHKHSRVREEVVNICICSLLTYPSEDFDLPKLSF DLAPALVDSKRRVRQAALEAFAVLASSMGSGKT SILFKAVDTVELQDNGDGVMNAVQARLARKTLP RLTEQGFVEYAVLMPSSAGGRSNHLAHGADTD WLLAGNRTQSAHCHCGDHVRDSMHIYGSYSPTI CTRRVLSAGKGKNKLPWENEQPGIMGENQTSTS KDIEQFSTYDFIPSAKLKLSQGMPVNDDLCFSRK RVSRNLFQNSRDFNPDCLPLCAAGTTGTHQTNLS GKCAQLGFSQICGKTGSVGSDLQFLGTTSSHQEK

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				VYASLNFGSKTQQTFGSQTECTSSNGQNPSPGAY ILPSYPVSSPRTSPKHTSPLIISPKKSQDNSVNFSNS WPLKSFEGLSKPKSHRRSLSAQKSS\DPTGR\NHG \ENSQEKPP\VQLTPAL\VRSPSSRRGLNGTKPVPPI P\RGISLLPDKADLSTVGHKKKKEPDDIWKCEKDS LPIDLSELNFKDKDLDQEEMHSSLRSLRNSAAKK RAKLSGSTSDLESPDSAMKLDLTMDSPSLSSSPNI NSYSESGVYSQESLTSSLSTTPQGKRIMSDIFPTFG SKPCPTRLSSAKKKISHIAEQSPSAGSSSNPQQISS FDFTTTKALSEDSVVVVGKGVFGSLSSAPATCSQ SVISSVENGDTFSIKQSIEPPSGIYGRSVQQNISSYL DVENEKDAKVSISKSTYNKMRQKRKEEKELFHN KDCEKKEKNSWERMRHTGTEKMASESETPTGAI SQYKERMPSVTHSPEIMDLSELRPFSKPEIALTEA LRLLADEDWEKKIEGLNFIRCLAAFHSEILNTKL HETNFAVVQEVKNLRSGVSRAAVVCLSDLFTYL KKSMDQELDTTVKVLLHKAGESNTFIREDVDKA LRAMVNNVTPARAVVSLINGGQRYYGRKMLFF MMCHPNFEKMLEKYVPSKDLPYIKDSVRNLQQK GLGEIPLDTPSAKGRRSHTGSVGNTRSSSVSRDA FNSAERAVTEVREVTRKSVPRNSLESAEYLKLIT GLLNAKDFRDRINGIKQLLSDTENNQDLVVGNIV KIFDAFKSRLHDSNSKVNLVALETMHKMIPLLRD HLSPIINMLIPAIVDNNLNSKNPGIYAAATNVVQA LSQHVDNYLLLQPFCTKAQFLNGKAKQDMTEKL ADIVTELYQRKPHATEQKVLVVLWHLLGNMTN SGSLPGAGGNIRTATAKLSKALFAQMGQNLLNQ AASQPPHIKKSLEELLDMTILNEL
3517	A	1449	252	QDLKPVLDREYLAIYLKMVFFTCNACGESVKKI QVEKHVSVCRNCECLSCIDCGKDFWGDDYKNH VKCISEDQKYGGKGY/EKVKTHKGD/ASKQQAW IQKISELIK\RPNVSPKVRELLEQISAFDNVPQ\KK AKFQNWMKNSLKVHNESILDQVWNIFSEASNSE PVNKEQDQRPLHPVANPHAEISTKVPASKVKDA VEQQGEVKKNKRERKEERQKKRKREKKELKLE NHQENSRNQKPKKRKKGQEADLEAGGEEVPEA NGSAGKRSKKKKQRKDSASEEEARVGAGKRKR RHSKVETDSKKKKMKLPEHPEGGEPEDDEAPAK GKFNWKGTIKAILKQAPDNEITIKKLRKKVLAQY YTVTDEHHRSEEELLVIFNKKISKNPTFKLLKDK VKLVK
3518	A	3	635	APDSNARNDHFDACSLRVQAGLSSAGPALGNSG LAALMASPSKAVIVPGNGGGDVTTHGWYGWVK KELEKIPGFQCLAKNMPDPITARESIWLPFMETEL HCDEKTIIIGHSSGAIAAMRYAETHRVYAIVLVSA YTSDLGDENERASGYFTRPWQWEKIKANCPYIV QFGSTDDPFLPWKEQQEVAD\SWKPNCTNSLTV ATFRTQSFMN
3519	A	81	2277	VRETRREMAMAMSDSGASRLRRQLESGGFEARL YVKQLSQQSDGDRDLQEHRQRIQALAEETAQNL KRNVYQNYRQFIETAREISYLESEMYQLSHLLTE QKSSLESIPLTLLPAAAAAGAAAASGGEEGVGGA GGRDHLRGQAGFFSTPGGASRDGSGPGEEGKQR TLTTLLEKVEGCRHLLETPGQYLVYNGDLVEYD ADHMAQLQRVHGFLMNDCLLVATWLPQRRGM

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				YRYNALYSLDGLAVVNVKDNPPMKDMFKLLMF PENRIFQAENAKIKREWLEVLEDTKRALSEKRRR EQEEAAAPRGPPQVTSKATNPFEDDEEEEPAVPE VEEEKVDLSMEWIQELPEDLDVCIAQRDFEGAV DLLDKLNHYLEDKPSPPPVKELRAKVEERVRQL TEVLVFELSPDRSLRGGPKATRRAVSQLIRLGQC TKACELFLRNRAAAVHTAIRQLRIEGATLLYIHK LCHVFFTSLLETAREFEIDFAGTDSGCYSAFVVW ARSAMGMFVDAFSKQVFDSKESLSTAAECVKVA KEHCQQLGDIGLDLTFIIHALLVKDIQGALHSYK EIIIEATKHRNSEEMWRRMNLMTPEALGKLKEE MKSCGVSNFEQYTGDDCWVNLSYTVVAFTKQT MGFLEEALKLYFPELHMVLLESLVEIILVAVQHV DYSLRCEQDPEKKAFIRQNASFLYETVL\PVVEK RFEEGVGKPAKQLQDLRNASRLIRVNPESTTSVV
3520	A	1706	540	FVAHLAWPWRADGDMEDGVLNEGFLVKRGHIV HNWKARWFILRQNTLVYYKLEGGRRVTPPKGRI LLDGCTITCPCLEYENRPLLIKLKTQTSTEYFLEA CSREE/RRDAWAFE\ITGAIHAGQARGKVQQLHS LRNSFKLPPHISLHRIVDKMHDSNTGIRSSPNMEQ GSTYKKTFLGSSLVDWLISNSFTASRLEAVTLAS MLMEENFLRPVGVRSMGAIRSGDLAEQFLDDST ALYTFAESYKKKISPKEEISLSTVELSGTVVKQGY LAKQGHKRKNWKVRRFVLRKDPAFLHYYDPSK EENRPVGGFSLRGSLVSALEDNGVPTGVKGNVQ GNLFKVITK\DDTHYYIQA\SSKAE\RAE\WIGSLS KSLNMNKDPEGTPDSLPSLPR
3521	A	3	3063	HASVSLSLGCPRPCADTPGPQPQPMDLRVGQRPP VEPPPEPTLLALQRPQRLHHHLFLAGLQQQRSVE PMRVKMELPACGATLSLVPSLPAFSIPRHQSQSST PCPFLGCRPCPQLSMDTPMPELQEAPQEQELRQL LHKDKSKRSAVASSVVKQKLAEVILKKQQAALE RTVHPNSPGIPYRTLEPLETEGATRSMLSSFLPPV PSLPSDPPEHFPLRKTVSEPNLKLRYKPKKSLERR KNPLLRKESAPPSLRRRPAETLGDSSPSSSSTPAS GCSSPNDSEHGPNPILGSEALLGQRLRLQETSVAP FALPTVSLLPAITLGLPAPARADSDRRTHPTLGPR GPILGSPHTPLFLPHGLEPEAGGTLPSRLQPILLLD PSGSHAPLLTVPGLGPLPFHFAQSLMTTERLSGSG LHWPLSRTRSEPLPPSATAPPPPGPMQPRLEQLKT HVQVIKRSAKPSEKPRLRQIPSAEDLETDGGGPG QVVDDGLEHRELGHGQPEARGPAPLQQHPQVLL WEQQRLAGRLPRGSTGDTVLLPLAQGGHRPLSR AQSSPAAPASLSAPEPASQARVLSSSETPARTLPF TTGLIYDSVMLKHQCSCGDNSRHPEHAGRIQSIW SRLQERGLRSQCECLRGRKASLEELQSVHSERHV LLYGTNPLSRLKLDNGKLAGLLAQRMFVMLPCG GVGVDTDTIWNELHSSNAARWAAGSVTDLAFK VASRELKNGFAVVRPPGHHADHSTAMGFCFFNS VAIACRQLQQQSKASKILIVDWDVHHGNGTQQT FYQDPSVLYISLHRHDDGNFFPGSGAVDEVGAGS GEGFNVNVAWAGGLDPPMGDPEYLAAFRIVVM PIAREFSPDLVLVSAGFDAAEGHPAPLGGYHVSA KCFGYMTQQLMNLAGGAVVLALEGGHDLTAIC DASEACVAALLGNRVDPLSEEGWKQKPNLNAIR

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				SLEA\VIRVHSKYWGCMQRLASCPDSWVPRVPG ADKEEVEAVTALASLSVGILAEDRPSEQLVEEEE PMNL
3522	A	9	602	KMAALGEPVRLERDICRAIELLEKLQRSGEVPPQ KLQALQRVLQSEFCNAVREVYEHVYETVDISSSP EVRANATAKATVAAFAASEGHSHPRVVELPKTE EGLGFNIMGGKEQNSPIYISRIIP/GGIADRHGGLK RGDQLLSVNGVSVEGEHHEKAVELLKAAQGKV KLVVRYTPKVLEEMESRFEKMRSAKRRQQT
3523	A	645	1465	IMAETSLLEAGASAASTAAALENLQVEASCSVCL EYLKEPVIIECGHNFCKACITRWWEDLERDFPCP VCRKTSRYRSLRPNRQLGSMVEIAKQL\RPSSGRS GMRASAPQHHEALSLFCYEDQEAVCLICAISHTH RAHTVVPLDDATQEYKEKLQKCLEA\LNQKLQEI TRCKSSEEKKPGELKRLVESRRQQILREFEELHRR LDEEQQVLLSRLEEEEQDILQRLRENAAHLGDKR RDLAHLAAEVEGKCLQSGFEMLKVRPLPLHSPS G
3524	A	3	698	PMVRHEAGEALGAIGDPEVLEILKQYSSDPVIEV AETCQLAVRRLEWLQQHGGEPAAGPYLSVDPAP PAEER\DVGRLREALLDESRPLFERYRAMFALRN AGGEEAALALAEGLHCGSALFRHEVGYVLGQLQ HEAAVPQLAAALARCTENPMVRHECAEALGAIA RPACLAALQAHADDPERVVRE\SCKVALDMYEH ETGRAFQYADGLEQLRGAPSLGPNPHPELPEDS
3525	A	1452	694	EGLQRPEYLVASAAGFQGLAWGGEGRGRAGCS SSGFRDAEPLLLSCPGRNEPLKKERLKWKSDYP MTDGQLRSKRDEFWDTAPAFEGRKEIWDALKA AAYAAEANDHELAQAILDGASITLPHGTLCECY DELGNRYQLPIYCLSPPVNLLLEHTEEESLEPPEP PPSVRREFPLKVRLSTGKDVRLSASLPDTVGQLK RQLHAQE/GTPKPSWQRWFFSGKLLTDRTRLQET KIQKDFVIQVIINQPPPPQD
3526	A	123	3441	PGNEGLGLAADHNEDLGHLSADAPWPAVTMAP RKRSHHGLGFLCCFGGSDIPEINLRDNHPLQFME FSSPIPNAEELNIRFAELVDELDLTDKNREAMFAL PPEKKWQIYCSKKKEQEDPNKLATSWPDYYIDRI NSMAAMQSLYAFDEEETEMRNQVVEDLKTALR TQPMRFVTRFIELEGLTCLLNFLRSMDHATCESRI HTSLIGCIIALMNNSQGRAHVLAQPEAISTIAQSL RTENSKTKVAVLEILGAVCLVPGGHKKVLQAML HYQVYAAERTRFQTLLNELDRSLGRYRDEVNLK TAIMSFINAVLNAGAGEDNLEFRLHLRYEFLMLG IQPVIDKLRQHENAILDKHLDFFEMVRNEDDLEL ARRFDMVHIDTKSASQMFELIHKKLKYTEAYPC LLSVLHHCLQMPYKRNGGYFQQWQLLDRILQQI VLQDERGVDPDLAPLENFNVKNIVNMLINENEV KQWRDQAEKFRKEHMELVSRLERKERECETKTL EKEEMMRT\LNKMKDKLARESQELRQARGQVA ELVAQLSELSTGPVSSPPPPGGPLTLSSSMTTNDL PPPPPPLPFACCPPPPPPPLPPGGPPTPPGAPPCLG MGLPLPQDPYPSSDVPLRKKRVPQPSHPLKSFNW VKLNEERVPGTVWNEIDDMQVFRILDLEDFEKM FSAYQRHQELITNPSQQKELGSTEDIYLASRKVK ELSVIDGRRAQNCIILLSKLKLSNEEIRQAILKMD

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				EQEDLAKDMLEQLLKFIPEKSDIDLLEEHKHEIER MARADRFLYEMSRIDHYQQRLQALFFKKKFQER LAEAKPKVEAILLASRELVRSKRLRQMLEVILAI GNFMNKGQRGGAYGFRVASLNKIADTKSSIDRN ISLLHYLIMILEKHFPDILNMPSELQHLPEAAKVN LAELEKEVGNLRRGLRAVEVELEYQRRQVREPS DKFVPVMSDFITVSSFSFSELEDQLNEARDKFAK ALMHFGEHDSKMQPDEFFGIFDTFLQAFSEARQD LEAMRRRKEEEERRARMEAMLKEQRERERWQR QRKVLAAGSSLEEGGEFDDLVSALRSGEVFDKD LCKLKRSRKRSGSQALEVTRERAINRLNY
3527	A	1445	714	LLGTRMLAGQLEARDPKEGTHPEDPCPGAGAV MEKTAVAAEVLTEDCNTGEMPPLQQQIIRLHQE LGRQKSLWADVHGKLRSHIDALREQNMELREKL RALQLQRWKARKKSAASPHAGQESHTLALEPAF GKISPLSADEETIPKYAGHKN\QSGHSSWGQRSSS NNSAPPKPMSLKIERISSWKTPPQENRDKNLSRR RQDRRATPTGRPTPCAERRG\VSEDGKVASDTCV TLHWPLGKFRFR
3528	A	484	1777	RISKIQVYYSTGYSSRKMNPTLGLAIFLAVLLTVK GLLKPSFSPRNYKALSEVQGWKQRMAAKELAR QNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFS MLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFH YIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLE DAKNFYSAETILTNFQNLEMAQKQINDFI/ESKTH GKINNLIENIDPGTVMLLANYIFFRARWKHEFDP NVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDD KLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQV DTFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKT LSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVNKA ELKMDERGTEGAAGTGAQTLPMETPLVVKIDKP YLLLIYSEKIPSVLFLGKIVNPIGK
3529	A	1	5684	VSSVSHENPTEVFEDGENPPSSRSSESGFTEFIQY QADRTDDIDRELSEGQGAAAIPIGSTSSETETAST VGSEETIIQTPSVVTQGTATRSRKTAQKTAMQCC LEYVQQFLTRLINLYIIQNNSFSQSLATEHQGDLG REQGETSKWDRNSQGDVKEKNISKQKTSKEYLS AFLAACQLFLECSSFPVYIAEGNHTSELRSEKLET DCEHVQPPQWLQTLMNACSQASDFSVQSVAISL VMDLVGLTQSVAMVTGENINSVEPAQPLSPNQG RVAVVIRPPLTQGNLRYIAEKTEFFKHVALTLWD QLGDGTPQHHQKSVELFYQLHNLVPSSSICEDVI SQQLTHKDKKIRMEAHAKFAVLWHLTRDLHINK SSSFVRSFDRSLFIMLDSLNSLDGSTSSVGQAWL NQVLQRHDIARVLEPLLLLLLHPKTQRVSVQRV QAERYWNKSPCYPGEESDKHFMQNFACSNVSQ VQLITSKGNGEKPLTMDEIENFSLTVNPLSDRLSL LSTSSETIPMVVSDFDLPDQQIEILQSSDSGCSQSS AGDNLSYEVDPETVNAQEDSQMPKESSPDDDVQ QVVFDLICKVVSGLEVESASVTSQLEIEAMPPKC SDIDPDEETIKIEDDSIQQSQNALLSNESSQFLSVS AEGGHECVANGISRNSSSPCISGTTHTLHDSSVAS IETKSRQRSHSSIQFSFKEKLSEKVSEKETIVKESG KQPGAKPKVKLARKKDDDKKKSSNEKLKQTSV FFSDGLDLENWYSCGEGDISEIESDMGSPGSRKSP

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				NFNIHPLYQHVLLYLQLYDSSRTLYAFSAIKAILK TNPIAFVNAISTTSVNNAYTPQLSLLQNLLARHRI SVMGKDFYSHIPVDSNHNFRSSMYIEILISLCLYY MRSHYPTHVKVTAQDLIGNRNMQMMSIEILTLL FTELAKVIESSAKGFPSFISDMLSKCKVQKVILHC LLSSIFSAQKWHSEKMAGKNLVAVEEGFSEDSLI NFSEDEFDNGSTLQSQLLKVLQRLIV\LEHRVM\T IPEE\NETGFDFVVS\DLEHISPHQPMTSLQYLHAQ SITCQGMFLCAVIRA\LHQHCACKMHPQWIGLIT STLPYMGKVLQRVVVSVTLQLCRNLDNLIQQYK YETGLSDSRPLWMASIIPPDMILTLLEGITAIIHYC LLDPTTQYHQLLVSV.DQKHLFEARSGILSILHMI MSSVTLLWSILHQADSSEKMTIAASASLTTINLG ATKNLRQQILELLGPISMNHGVHFMAAIAFVWN ERRQNKTTTRTKVIPAASEEQLLLVELVRSISVM RAETVIQTVKEVLKQPPAIAKDKKHLSLEVCML QFFYAYIQRIPVPNLVDSWASLLILLKDSIQLSLP APGQFLILGVLNEFIMKNPSLENKKDQRDLQDVT HKIVDAIGAIAGSSLEQTTWLRRNLEVKPSPKIM VDGTNLESDVEDMLSPAMETANITPSVYSVHAL TLLSEVLAHLLDMVFYSDEKERVIPLLVNIMHYV VPYLRNHSAHNAPSYRACVQLLSSLSGYQYTRR AWKKEAFDLFMDPSFFQMDASCVNHWRAIMDN LMTHDKTTFRDLMTRVAVAQSSSLNLFANRDVE LEQRAMLLKRLAFAIFSSEIDQYQKYLPDIQERLV ESLRLPQVPTLHSQVFLFFRVLLLRMSPQHLTSL WPTMITELVQVFLLMEQELTADEDISRTSGPSVA GLETTYTGGNGFSTSYNSQRWLNLYLSACKFLD LALALPSENLPQFQMYRWAFIPEASDDSGLEVRR QGIHQREFKPYVVRLAKLLRKRAKKNPEEDNSG RTLGWEPGHLLLTICTVRSMEQLLPFFNVLSQVF NSKVTSRCGGHSGSPILYSNAFPNKDMKLENHKP CSSKARQKIEEMVEKDFLEGMIKT
3530	A	1	5684	VSSVSHENPTEVFEDGENPPSSRSSESGFTEFIQY QADRTDDIDRELSEGQGAAAIPIGSTSSETETAST VGSEETIIQTPSVVTQGTATRSRKTAQKTAMQCC LEYVQQFLTRLINLYIIQNNSFSQSLATEHQGDLG REQGETSKWDRNSQGDVKEKNISKQKTSKEYLS AFLAACQLFLECSSFPVYIAEGNHTSELRSEKLET DCEHVQPPQWLQTLMNACSQASDFSVQSVAISL VMDLVGLTQSVAMVTGENINSVEPAQPLSPNQG RVAVVIRPPLTQGNLRYIAEKTEFFKHVALTLWD QLGDGTPQHHQKSVELFYQLHNLVPSSSICEDVI SQQLTHKDKKIRMEAHAKFAVLWHLTRDLHINK SSSFVRSFDRSLFIMLDSLNSLDGSTSSVGQAWL NQVLQRHDIARVLEPLLLLLLHPKTQRVSVQRV QAERYWNKSPCYPGEESDKHFMQNFACSNVSQ VQLITSKGNGEKPLTMDEIENFSLTVNPLSDRLSL LSTSSETIPMVVSDFDLPDQQIEILQSSDSGCSQSS AGDNLSYEVDPETVNAQEDSQMPKESSPDDDVQ QVVFDLICKVVSGLEVESASVTSQLEIEAMPPKC SDIDPDEETIKIEDDSIQQSQNALLSNESSQFLSVS AEGGHECVANGISRNSSSPCISGTTHTLHDSSVAS IETKSRQRSHSSIQFSFKEKLSEKVSEKETIVKESG KQPGAKPKVKLARKKDDDKKKSSNEKLKQTSV

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				FFSDGLDLENWYSCGEGDISEIESDMGSPGSRKSP NFNIHPLYQHVLLYLQLYDSSRTLYAFSAIKAILK TNPIAFVNAISTTSVNNAYTPQLSLLQNLLARHRI SVMGKDFYSHIPVDSNHNFRSSMYIEILISLCLYY MRSHYPTHVKVTAQDLIGNRNMQMMSIEILTLL FTELAKVIESSAKGFPSFISDMLSKCKVQKVILHC LLSSIFSAQKWHSEKMAGKNLVAVEEGFSEDSLI NFSEDEFDNGSTLQSQLLKVLQRLIV\LEHRVM\T IPEE\NETGFDFVVS\DLEHISPHQPMTSLQYLHAQ SITCQGMFLCAVIRA\LHQHCACKMHPQWIGLIT STLPYMGKVLQRVVVSVTLQLCRNLDNLIQQYK YETGLSDSRPLWMASIIPPDMILTLLEGITAIIHYC LLDPTTQYHQLLVSVDQKHLFEARSGILSILHMI MSSVTLLWSILHQADSSEKMTIAASASLTTINLG ATKNLRQQILELLGPISMNHGVHFMAAIAFVWN ERRQNKTTTRTKVIPAASEEQLLLVELVRSISVM RAETVIQTVKEVLKQPPAIAKDKKHLSLEVCML QFFYAYIQRIPVPNLVDSWASLLILLKDSIQLSLP APGQFLILGVLNEFIMKNPSLENKKDQRDLQDVT HKIVDAIGAIAGSSLEQTTWLRRNLEVKPSPKIM VDGTNLESDVEDMLSPAMETANITPSVYSVHAL TLLSEVLAHLLDMVFYSDEKERVIPLLVNIMHYV VPYLRNHSAHNAPSYRACVQLLSSLSGYQYTRR AWKKEAFDLFMDPSFFQMDASCVNHWRAIMDN LMTHDKTTFRDLMTRVAVAQSSSLNLFANRDVE LEQRAMLLKRLAFAIFSSEIDQYQKYLPDIQERLV ESLRLPQVPTLHSQVFLFFRVLLLRMSPQHLTSL WPTMITELVQVFLLMEQELTADEDISRTSGPSVA GLETTYTGGNGFSTSYNSQRWLNLYLSACKFLD LALALPSENLPQFQMYRWAFIPEASDDSGLEVRR QGIHQREFKPYVVRLAKLLRKRAKKNPEEDNSG RTLGWEPGHLLLTICTVRSMEQLLPFFNVLSQVF NSKVTSRCGGHSGSPILYSNAFPNKDMKLENHKP CSSKARQKIEEMVEKDFLEGMIKT
3531	A	553	2470	LISPSPALSSQDPALSLKENLEDISGWGLPEARSK ESVSFKDVAVDFTQEEWGQLDSPQRALYRDVM LENYQNLLALGPPLHKPDVISHLERGEEPWSMQ REVPRGPCPEWELKAVPSQQQGICKEEPAQEPIM ERPLGGAQAWGRQAGALQRSQAAP\GR\RTCHG LGRP\VEEFPLRCPLFAQQRVPEGGPLLDTRKNV QATEGRTKAPARLCAGENASTPSEPEKFPQVRRQ RGAGAGEGEFVCGECGKAFRQSSSLTLHRRWHS REKAYKCDECGKAFTWSTNLLEHRRIHTGEKPFF CGECGKAFSCHSSLNVHQRIHTGERPYKCSACEK AFSCSSLLSMHLRVHTGEKPYRCGECGKAFNQR THLTRHHRIHTGEKPYQCGSCGKAFTCHSSLTVH EKIHSGDKPFKCSDCEKAFNSRSRLTLHQRTHTG EKPFKCADCGKGFSCHAYLLVHRRIHSGEKPFKC NECGKAFSSHAYLIVHRRIHTGEKPFDCSQCWKA FSCHSSLIVHQRIHTGEKPYKCSECGRAFSQNHCL IKHQKIHSGEKSFKCEKCGEMFNWSSHLTEHQRL HSEGKPLAIQFNKHLLSTYYVPGSLLGAGDAGLR DVDPIDALDVAKLLCVVPPRAGRNFSLGSKPRN
3532	A	3931	317	HRELQDSPSAEPPAGSMPLRHWGMARGSKPVGD GAQPMAAMGGLKVLLHWAGPGGGEPWVTFSES

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				SLTAEEVCIHIAHKVGITPPCFNLFALFDAQAQV WLPPNHILEIPRDASLMLYF\RHRFYSR\NWHGM NPREPAVYRCGPPGTEASSDQTAQGMQLLDPAS FEYLFEQGKHEFVNDVASLWELSTEEEIHHFKNE SLGMAFLHLCHLALRHGIPLEEVAKKTSFKDCIP RSFRRHIRQHSALTRLRLRNVFRRFLRDFQPGRLS QQMVMVKYLATLERLAPRFGTERVPVCHLRLLA QAEGEPCYIRDSGVAPTDPGPESAAGPPTHEVLV TGTGGIQWWPVEEEVNKEEGSSGSSGRNPQASL FGKKAKAHKAFGQPADRPREPLGAYFCDFRDIT HVGLKEHCVSIHRQDNKCLELSLPSRAAALSFVS LVDGYFRLTADSSHYLCHEVAPPRLVMSIRDGIH GPLLEPFVQAKLRPEDGLYLIHWSTSHPYRLILTV AQRSQAPDGMQSLRLRKFPIEQQDGAFVLEGWG RSFPSVRELGAALQGCLLRAGDDCFSLRRCCLPQ PGETSNLIIMRGARASPRTLNLSQLSFHRVDQKEI TQLSHLGQGTRTNVYEGRLRVEGSGDPEEGKMD DEDPLVPGRDRGQELRVVLKVLDPSHHDIALAF YETASLMSQVSHTHLAFVHGVCVRGPENIMVTE YVEHGPLDVWLRRERGHVPMAWKMVVAQQLA SALSYLENKNLVHGNVCGRNILLARLGLAEGTSP FIKLSDPGVGLGALSREERVERIPWLAPECLPGG ANSLSTAMDKWGFGATLLEICFDGEAPLQSRSPS EKEHFYQRQHRLPEPSCPQLATLTSQCLTYEPTQ RPSFRTILRDLTRLQPHNLADVLTVNPDSPASDPT VFHKRYLKKIRDLGEGHFGKVSLYCYDPTNDGT GEMVAVKALKADCGPQHRSGWKQEIDILRTLYH EHIIKYKGCCEDQGEKSLQLVMEYVPLGSLRDYL PRHSIGLAQLLLFAQQICEGMAYLHAQHYIHRDL AARNVLLDNDRLVKIGDFGLAKAVPEGHEYYRV REDGDSPVFWYAPECLKEYKFYYASDVWSFGVT LYELLTHCDSSQSPPTKFLELIGIAQGQMTVLRLT ELLERGERLPRPDKCPCEVYHLMKNCWETEASF RPTFENLIPILKTVHEKYQGQAPSVFSVC
3533	A	182	3465	FRWLDFFRGSINSQFEFGRKKENMTSPAKFKKDK EIIAEYDTQVKEIRAQLTEQMKCLDQQCELRVQL LQDLQDFFRKKAEIEMDYSRNLEKLAERFLAKT RSTKDQQFKKDQNVLSPVNCWNLLLNQVKRES RDHTTLSDIYLNNIIPRFVQVSEDSGRLFKKSKEV GQQLQDDLMKVLNELYSVMKTYHMYNADSISA QSKLKEAEKQEEKQIGKSVKQEDRQTPRSPDSTA NVRIEEKHVRRSSVKKIEKMKEKRQAKYTENKL KAIKARNEYLLALEATNASVFKYYIHDLSDLIDQ CCDLGYHASLNRALRTFLSAELNLEQSKHEGLD AIENAVENLDATSDKQRLMEMYNNVFCPPMKFE FQPHMGDMASQLCAQQPVQSELLQRCLQLQSRL STLKIENEEVKKTMEATLQTIQDIVTVEDFDVSD CFQYSNSMESVKSTVSETFMSKPSIAKRRANQQE TEQFYFTKMKEYLEGRNLITKLQAKHDLLQKTL GESQRTDCSLARRSSTVRKQDSSQAIPLVVESCIR FISRHGLQHEGIFRVSGSQVEVNDIKNAFERGEDP LAGDQNDHDMDSIAGVLKLYFRGLEHPLFPKDIF HDLMACVTMDNLQERALHIRKVLLVLPKTTLII MRYLFAFLNHLSQFSEENMMDPYNLAICFGPSL MSVPEGHDQVSCQAHVNELIKTIIIQHENIFPSPRE

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				LEGPVYSRGGSMEDYCDSPHGETTSVEDSTQDV TAEHHTSDDECEPIEAIAKFDYVGRTARELSFKK GASLLLYQRASDDWWEGRHNGIDGLIPHQYIVV QDTEDGVVERSSPKSEIEVISEPPEEKVTARAGAS CPSGGHVADIYLANINKQRKRPESGSIRKTFRSDS HGLSSSLTDSSSPGVGASCRPSSQPIMSQSLPKEG PDKCSISGHGSLNSISRHSSLKNRLDSPQIRKTAT AGRSKSFDNHRPMDPEVIAQDIEATMNSALNELR ELERQSSVKHTPDVVLDTLEPLKTSPVVAPTSEPS SPLHTQLLKDPEPAFQRSASTAGDIACAFRPVKS VKMAAPVKPPAT\RPKPT\VFPKTNATSPGVNSST SPQSTDKSCTV
3534	A	1	2640	FRRFVCPASRRPAAGLRDAASSAPRGMASEGPRE PESEGIKLSADVKPFVPRFAGLNVAWLESSEACV FPSSAATYYPFVQEPPVTEQKIYTEDMAFGASTFP PQYLSSEITLHPYAYSPYTLDSTQNVYSVPGSQY LYNQPSCYRGFQTVKHRNENTCPLPQEMKALFK KKTYDEKKTYDQQKFDSERADGTISSEIKSARGS HHLSIYAENSLKSDGYHKRTDRKSRIIAKNVSTS KPEFEFTTLDFPELQGAENNMSEIQKQPKWGPVH SVSTDISLLREVVKPAAVLSKGEIVVKNNPNESV TANAATNSPSCTRELSWTPMGYVVRQTLSTELS AAPKNVTSMINLKTIASSADPKNVSIPSSEALSSD PSYNKEKHIIHPTQKSKASQGSDLEQNEASRKNK KKKEKSTSKYEVLTVQEPPRIEDAEEFPNLAVAS ERRDRIETPKFQSKQQPQDNFKNNVKKSQLPVQL DLGGMLTALEKKQHSQHAKQSSKPVVVSVGAV PVLSKECASGERGRRMSQMKTPHNPLDSSAPLM KKGKQREIPKAKKPTSLKKIILKERQERKQRLQE NAVSPAFTSDDTQDGESGGDDQFPEQAELSGPEG MDELISTPSVEDKSEEPPGTELQRDTEASHLAPN HTTFPKIHSRRFRDYCSQMLSKEVDACVTDLLKE LVRFQDRMYQKDPVKAKTKRRLVLGLREVLKH LKLKKLKCVIISPNCEKIQSKGGLDDTLHTIIDYA CEQNIPFVFALNRKALGRSLNKAVPVSVVGIFSY DGAQDQFHKMVELTVAARQAYKTMLENVQQE LVGEP\SLRHLPAYPHRAPAALQKMAPQP/VKEK EEPHYIEIWKKHLEAYSGCTLELEESLEASTSQM MNLNL
3535	A	1747	983	LFQFQVCRSVLSPRAAGCTWSLAPRSRGAAGSPR RYRGPQPQPAPPSALPNSRPSPVASGREMVVLSV PAEVTVILLDIEGTTTPIAFVKDILFPYIEENVKEY LQTHWEEEECQQDVSLLRKQV\FADVVPAVRKW REAGMKVYIYSSGSVEAQKLLFGHSTEGDILELV DGHFDTKIGHKVESESYRKIADSIGCSTNNILFLT DVTREASAAEEADVHVAVVVRPGNAGLTDDEK TYYSLITSFSELYLPSST
3536	A	3	1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTS IESRGRPAASAGLRRDRCALRRWPLRRAPLARAT RRRAGSPRRCAPRPRACPQGWSRARHQPGGLCL LLLLLCQFMEDRSAQAGNCWLRQAKNGRCQVL YKTELSKEECCSTGRLSTSWTEEDVNDNTLFKW MIFNGGAPNCIPCKETCENVDCGPGKKCRMNKK NKPRCVCAPDCSNITWKGPVCGLDGKTYRNECA LLKARCKEQPELEVQYQGRCKKTCRDVFCPGSS

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				TCV\VDQTNNAYCVTCNRICPEPASSEQYLCGND GVTYS\SACHLRKATCLLGRSIGLAYEGKCIKAK SCEDIQCTGGKKCLWDFKVGRGRCSLCDELCPD SKSDEPVCASDNATYASECAMKEAACSSGVLLE VKHSGSCNSISEDTEEEEEDEDQDYSFPISSILEW
3537	A	285	2123	IGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRF LTSIPTGIPEDATTLYLQNNQINNAGIPSDLKNLL KVERIYLYHNSLDEFPTNLPKYVKELHLQENNIR TITYDSLSKIPYLEELHLDDNSVSAVSIEEGAFRD SNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIS TISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFF NLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQ DNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQ GIFDDLDNITQLILRNNPWYCGCKMKWVRDWL QSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELF DCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTK QPDIKNPKLTKDHQTTGSPSRKTITITVKSVTSDTI HISWKLALPMTALRLSWLKLGHSPAFGSITETIVT GERSEYLVTALEPDSPYKVCMVPMETSNLYLFD ETPVCIETETAPLRMYNPTTTLNREQEKEPYKNP NLPLAAIIGGAVALVTIALLALVCWYVHRNGSLF SRNCAYSKGRRRKDDYAEAGTKKDNSILEIRETS FQMLPISNEPISKEEFVIHTIFPPNGMNLYKNNH
3538	A	877	6184	WNVKPSLLVVQLFKFSDKEEHEQNDSISGKTGET GVEEMIATRKVEQDSKETVKLSHEDDHILEDAGS SDISSDAACTNPNKTENSLVGLPSCVDEVTECNL ELKDTMGIADKTENTLERNKIEPLGYCEDAESNR QLESTEFNKSNLEVVDTSTFGPESNILENAICDVP DQNSKQLNAIESTKIESHETANLQDDRNSQSSSV SYLESKSVKSKHTKPVIHSKQNMTTDAPKKIVAA KYEVIHSKTKVNVKSVKRNTDVPESQQNFHRPV KVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKK TLQDQTLVQIFKPLTHSLSDKSHAHPGCLKEPHH PAQTGHVSHSSQKQCHKPQQQAPAMKTNSHVK EELEHPGVEHFKEEDKLKLKKPEKNLQPRQRRSS KSFSLDEPPLFIPDNIATIRREGSDHSSSFESKYMW TPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDC VGLSLSQAQQMGEEDKEYVCVKCCAEEDKKTEI LDPDTLENQATVEFHSGDKTMECEKLGLSKHTT NDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKE STTVTCTGEKASKPGTHEKQEMKKKKV\EKGVL NVHPAASASKPSADQIRQSVRHSLKDILMKRLTD SNLKVPEEKAAKVATKIEKELFSFFRDTDAKYKN KYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIR MSPEELASKELAAWRRRENRHTIEMIEKEQREVE RRPITKITHKGEIEIESDAPMKEQEAAMEIQEPAA NKSLEKPEGSEK\RKEEVDSMSKDTTSQHRQHLF DLNCKICIGRMAPPVDDLSPKKVKVVVGVARKH SDNEAESIADALSSTSNILASEFFEEEKQESPKSTF SPAPRPEMPGTVEVESTFLARLNFIWKGFINMPS VAKFVTKAYPVSGSPEYLTEDLPDSIQVGGRISPQ TVWDYVEKIKASGTKEICVVRFTPVTEEDQISYT LLFAYFSSRKRYGVAANNMKQVKDMYLIPLGAT DKIPHPLVPFDGPGLELHRPNLLLGLIIRQKLKRQ

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				HSACASTSHIAETPESAPPIALPPDKKSKIEVSTEE APEEENDFFNSFTTVLHKQRNKPQQNLQEDLPTA VEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLE LANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQ NTVKEIPFLNEQTNSKIEKTDNVEVTDGENKEIK VKVDNISESTDKSAEIETSVVGSSSISAGSLTSLSL RGKPPDVSTEAFLTNLSIQSKQEETVESKEKTLKR QLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGN VSCSENLVANTARSPQFINLKRDPRQAAGRSQPV TTSESKDGDSCRNGEKHMLPGLSHNKEHLTEQIN VEEKLCSAEKNSCVQQSDNLKVAQNSPSVENIQT SQAEQAKPLQEDILMQNIETVHPFRRGSAVATSH FEVGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRP QQPNLQHLKSSPPGFPFPGPPNFPPQSMFGFPPHL PPPLLPPPGFG\FA\QNPMVPWPPVV\HLP\GQPQR MMGPLSQASRYIGPQNFYQVKDIRRPERRHSDP WGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKR ERHEKEWEQESERHRRRDRSQDKDRDRKSREEG HKDKERARLSHGDRGTDGKASRDSRNVDKKPD KPKSEDYEKDKEREKSKHREGEKDRDRYHKDR DHTDRTKSKR
3539	A	157	1769	GSWTVELSLKPSASPSLKWVCLPGAAAVNKHRS GAGGLIRSLIQCTWAPAGPARRGGRGIEDFPYLF FQLTHCQQRICSVTQAGVQWCDHSSLQPQTPGL NQSSHLSLLSSRDYRMLSSFNEWFWQDRFWLPP NVTWTELEDRDGRVYPHPQDLLAALPLALVLLA MRLAFERFIGLPLSRWLGVRDQTRRQVKPNATL EKHFLTEGHRPKEPQLSLLAAQCGLTLQQTQRW FRRRRNQDRPQLTKKFCEASWRFLFYLSSFVGGL SVLYHESWLWAPVMCWDRYPNQLTLSCPAADS EA\SLYWWYLLELGFYLSLLIRLPFDVKRKGGGP SSIKPRPHYDPPSTA\DFKEQVIHHFVAVILMTFSY SANLLRIGSLVLLLHDSSDYLLEACKMVNYMQY QQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESI SNRGPFFGYYFFNGLLMLLQLLHVFWSCLILRML YSFMKKGQMEKDIRSDVEESDSSEEAAAAQEPL QLKNGTAGGPRPAPTDGPRSRVAGRLTNRHTTA T
3540	A	267	1397	SPAGYCHSGLLPGCSRSA/CADLAKHQELPGKKL LSEKKLKRYFVDYRRVLVCGGNGGAGASCFHSE PRKEFGGPDGGDGGNGGHVILRVDQQVKSLSSV LSRYQGFSGEDGGSKNCFGRSGAVLYIRVPVGTL VKEGGRVVADLSCVGDEYIAALGGAGGKGNRF FLANNNRAPVTCTPGQPGQQRVLHLELKTVAHA GMVGFPNAGKSSLLRAISNARPAVASYPFTTLKP HVGIVHYEGHLQIAVADIPGIIRGAHQNRGLGSA FLRHIERCRFLLFVVDLSQPEPWTQVDDLKYELE MYEKGLSARPHAIVANKIDLPEAQANLSQLRDH LGQEVIVLSALTGENLEQLLLHLKVLYDAYAEA ELGQGRQPLRW
3541	A	1	8008	DTQVSETLKRFAGKVTTASVKERREILSELGKCV AGKDLPEGAVKGLCKLFCLTLHRYRDAASRRAL QAAIQQLAEAQPEATAKNLLHSLQSSGIGSKAGV PSKSSGSAALLALTWTCLLVRIVFPSRAKRQGDI WNKLVEVQCLLLLEVLGGSHKHAVDGAVKKLT

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				KLWKENPGLVEQYLSAILSLEPNQNYAGMLGLL VQFCTSHKEMDVVSQHKSALLDFYMKNILMSK VKPPKYLLDSCAPLLRYLSHSEFKDLILPTIQKSL LRSPENVIETISSLLASVTLDLSQYAMDIVKGLAG HLKSNSPRLMDEAVLALRNLARQCSDSSAMESL TKHLFAILGGSEGKLTVVAQKMSVLSGIGSVSHH VVSGPSSQVLNGIVAELFIPFLQQEVHEGTLVHA VSVLALWCNRFTMEVPKKLTEWFKKAFSLKTST SAVRHAYLQCMLASYRGDTLLQALDLLPLLIQT VEKAASQSTQVPTITEGVAAALLLLKLSVADSQA EAKLSSFWQLIVDEKKQVFTSEKFLVMASEDAL CTVLH\LTERLFLDHPHRLTGNKVQQYHRALVA VLLSRTWHVRRQAQQTVRKLLSSLGGFKLAHGL LEELKTVLSSHKVLPLEALVTDAGEVTEAGKAY VPPRVLQEALCVISGVPGLKGDVTDTEQLAQEM LIISHHPSLVAVQSGLWPALLARMKIDPEAFITRH LDQIIPRMTTQSPLNQSSMNAMGSLSVLSPDRVL PQLISTITASVQNPALRLVTREEFAIMQTPAGELY DKSIIQSAQQDSIKKANMKRENKAYSFKEQIIELE LKEEIKKKKGIKEEVQLTSKQKEMLQAQLDREA QVRRRLQELDGELEAALGLLDIILAKNPSGLTQYI PVLVDSFLPLLKSPLAAPRIKNPFLSLAACVMPSR LKALGTLVSHVTLRLLKPECVLDKSWCQEELSV AVKRAVMLLHTHTITSRVGKGEPGAAPLSAPAFS LVFPFLKMVLTEMPHHSEEEEEWMAQILQILTVQ AQLRASPNTPPGRVDENGPELLPRVAMLRLLTW VIGTGSPRLQVLASDTLTTLCASSSGDDGCAFAE QEEVDVLLCALQSPCASVRETVLRGLMELHMVL PAPDTDEKNGLNLLRRLWVVKFDKEEEIRKLAE RLWSMMGLDLQPDLCSLLIDDVIYHEAAVRQAG AEALSQAVARYQRQAAEVMGRLMEIYQEKLYR PPPVLDALGRVISESPPDQWEARCGLALALNKLS QYLDSSQVKPLFQFFVPDALNDRHPDVRKCMLD AALATLNTHGKENVNSLLPVFEEFLKNAPNDAS YDAVRQSVVVLMGSLAKHLDKSDPKVKPIVAKL IAALSTPSQQVQESVASCLPPLVPAIKEDAGGMIQ RLMQQLLESDKYAERKGAAYGLAGLVKGLGILS LKQQEMMAALTDAIQDKKNFRRREGALFAFEM LCTMLGKLFEPYVVHVLPHLLLCFGDGNQYVRE AADDCAKAVMSNLSAHGVKLVLPSLLAALEEES WRTKAGSVELLGAMAYCAPKQLSSCLPNIVPKL TEVLTDSHVKVQKAGQQALRQIGSVIRNPEILAI APVLLDALTDPSRKTQKCLQTLLDTKFVHFIDAP SLALIMPIVQRAFQDRSTDTRKMAAQIIGNMYSL TDQKDLAPYLPSVTPGLKASLLDPVPEVRTVSAK ALGAMVKGMGESCFEDLLPWLMETLTYEQSSV DRSGAAQGLAEVMAGLGVEKLEKLMPEIVATAS KVDIAPHVRDGYIMMFNYLPITFGDKFTPYVGPII PCILKALADENEFVRDTALRAGQRVISMYAETAI ALLLPQLEQGLFDDLWRIRFSSVQLLGDLLFHISG VTGKMTTETASEDDNFGTAQSNKAIITALGVERR NRVLAGLYMGRSDTQLVVRQASLHVWKIVVSN TPRTLREILPTLFGLLLGFLASTCADKRTIAARTL GDLVRKLGEKILPEIIPILEEGLRSQKSDERQGVCI GLSEIMKSTSRDAVLYFSESLVPTARKALCDPLE

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				EVREAAAKTFEQLHSTIGHQALEDILPFLLKQLD DEEVSEFALDGLKQVMAIKSRVVLPYLVPKLTTP PVNTRVLAFLSSVAGDALTRHLGVILPAVMLAL KEKLGTPDEQLEMANCQAVILSVEDDTGHRIIIE DLLEATRSPEVGMRQAAAIILNTYCSRSKADYTS HLRSLVSGLIRLFNDSSPVVLEESWDALNAITKK LDAGNQLALIEELHKEIRLIGNESKGEHVPGFCLP KKGVTSILPVLREGVLTGSPEQKEEAAKALGLVI RLTSADALRPSVVSITGPLIRILGDRFSWNVKAAL LETLSLLLAKVGIALKPFLPQLQTTFTKALQDSNR GVRLKAADALGKLISIHIKVDPLFTELLNGIRAME DPGVRDTMLQALRFVIQGAGAKVDAVIRKNIVS LLLSMLGHDEDNTRISSAGCLGELCAFLTEEELS AVLQQCLLADVSGIDWMVRHGRSLALSVAVNV APGRLCAGRYSSDVQEMILSSATADRIPIAVSGV RGMGFLMRHHIETGGGQLPAKLSSLFVKCLQNP SSDIRLVAEKMIWWANKDPLPPLDPQAIKPILKA LLDNTKDKNTVVRAYSDQAIVNLLKMRQGEEVF QSLSKILDVASLEVLNEVNRRSLKKLASQADSTE QVDDTILT
3542	A	62	1130	PWNPQDFPGNRGLMG\QKGEIGPP\GQQGKKGAP GMP\GLMGSNGSPGQPGTPGSKGSKGEPGIQGMP GASGLKGEPGATGSPGEPGYMGLPGIQGKKGDK GNQGEKGIQGQKGENGRQGIPGQQGIQGHHGAK GERGEKGEPGVRGAIGSKGESGVDGLMGPAGPK GQPGDPGPQGPPGLDGKPGREFSEQFIRQVCTDV IRAQLPVLLQSGRIRNCDHCLSQHGSPGIPGPPGPI GPEGPRGLPGLPGRDGVPGLVGVPGRPGVRGLK GLPGRNGEKGSQGFGYPGEQGPPGPPGPEGPPGI SKEGPPGDPGLPGKDGDHGKPGIQGQPGPPGICD PSLCFSVIARRDPFRKGPNY
3543	A	654	194	PARSLEKMKASVVLSLLGYLVVPSGAYILGRCTV AKKLHDGGLDYFERYSLENWVCLAYFESKFNPS\ AIYENTREGYTGFGLFQMRGSDWCGDHGRNRC HMSCSALLNPNLEKTIKCAKTIVKGKEGMGAWP TWSRYCQYSDTLARWLDGCKL
3544	A	2	1074	SCRLAAGRLAQWLLRASRSGMLRAGWLRGAAA LALLLAARVVAAFEPITVGLAIGAASAITGYLSY NDIYCRFAECCREERPLNASALKLDLEEKLFGQH LATEVI\FKALTGFRNNKNPKKPLTLSLHGWAGT GKNFVSQMGAENLHPKGLKSNFVHLFVSTLHFP HEQKIKLYQDQLQKWIRGNVSACANSVFIFDEM DKL\HPGIIE\AIKPFLDYYEHVERVSYR\KAIFIFLS NAGGDLITKTALDFWRAGRKREDIQLKDLEPVL SVGVFNNKHSGLWHSGLIDKNLIDYFIPFLPLEYR HVKMCVRAEMRARGSAIDEDIVTRVAEEMTFFP\ RDEKIYSDKGCKTVQSRLDFH
3545	A	3	273	SAQGRSWGRFYRQIKRHPGIIPMIGLICLGMGSA ALYLLRLALRSPDVW*SWDRKNNPEPWNRLSPN DQYKFLAVSTDYKKLKKDRPDF
3546	A	23	591	ALSTETRTPDMRRLLLVTSLVVVLLWEAGAVPA PKVPIKMQVKHWPSEQDPEKAWGARVVEPPEK DDQLVVLFPVQKPKLLTTEEKPRGQGRGPILPGT KAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQG EERPRLWVMPNHQVLLGPEEDQDHIYHPQ*GSR

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				GHHCPRPVPRPRLLGLGPSLPCPS
3547	A	23	591	ALSTETRTPDMRRLLLVTSLVVVLLWEAGAVPA PKVPIKMQVKHWPSEQDPEKAWGARVVEPPEK DDQLVVLFPVQKPKLLTTEEKPRGQGRGPILPGT KAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQG EERPRLWVMPNHQVLLGPEEDQDHIYHPQ*GSR GHHCPRPVPRPRLLGLGPSLPCPS
3548	A	3	1641	TWLPSVPAEEVQQPEMAAVLNAERLEVSVDGLT LSPDPEERPGAEGAPLAAATAATALATWIRSRPG RLRGTARSPGRRAAGGAAEEARRLEQRWGFGLE ELYGLALRFFKEKDGKAFHPTYEEKLKLVALHK QVLMGPYNPDTCPEVGFFDVLGNDRRREWAAL GNMSKEDAMVEFVKLLNRCCHLFSTYVASHKIE KEEQEKKRKEEEERRRREEEERERLQKEEEKRRR EEEERLRREEEERRRIEEERLRLEQQKQQIMAAL NSQTAVQFQQYAAQQYPGNYEQQQILIRQLQEQ HYQQYMQQLYQVQLAQQQAALQKQQEVVVAG SSLPTSSKVECNCTQVI*CQFNRQAKTHTDSSEKE LEPEAAEEALENGPKESLPVIAAPSMWTRPQIKD FKEKIQQDADSVITVGRGEVVTVRVPTHEEGSYL FWEFATDNYDIGFGVYFEWTDSPNTAVSVHVSE SSDDDEEEEENIGCEEKAKKNANKPLLDEIVPVY RRDCHEEVYAGSHQYPGRGVYLLKFDNSYSLW RSKSVYYRVYYTR
3549	A	1837	3593	PAVLVLEPASQSRKQQNTASATAQHWSAQIHKE SFLAPVFTKDEQKHRRPYEFEVERDAKARGLEQF SATHGHTPIILNGWHGESAMDLSCSSEGSPGATS PFPVSASTPKIGAISSLQGALGMDLSGILQAGLIHP VTGQIVNGSLRRDDAATRRRRGRRKHVEGGMD LIFLKEQTLQAGILEVHEDPGQATLSTTHPEGPGP ATSAPEPATAASSQAEKSIPSKSLLDWLRQQADY SLEVPGFGANFSDKPKQRRPRCKEPGKLDVSSLS GEERVPAIPKEPGLRGFLPENKFNHTLAEPILRDT GPRRRGRRPRSELLKAPSIVADSPSGMGPLFMNG LIAGMDLVGLQNMRNMPGIPLTGLVGFPAGFAT MPTGEEVKSTLSMLPMMLPGMAAVPQMFGVGG LLSPPMATTCTSTAPASLSSTTKSGTAVTEKTAE DKPSSHDVKTDTLAEDKPGPGPFSDQSEPAITTSS PVAFNPFLIPGVSPGLIYPSMFLSPGMGMALPAM QQARHSEIVGLESQKRKKKKTKGDNPNSHPEPA PSCEREPSGDENCAEPSAPLPAEREHGAQAGEGA LKDSNNDTN
3550	A	287	39	QLNLNKIATSQKHRDFVAESVGEKPVGSLAGIGE VMDKKLEEGCFDKAYVVLGQFLVLKKDEDLF*E WLRDTGGARTRGSRE
3551	A	21	3925	GDLLEVGLPPGLEFPRGICLRGLRRTMSLDFGSV ALPVQNEDEEYDEEDYEREKELQQLLTDLPHDM LDDDLSSPELQYSDCSEDGTDGQPHHPEQLEMS WNEQMLPKSQSVNGPSCQGLEPYNKVTYKPYQS SAQNNGSPAQEITGSDTFEGLQQQFLGANENSAE NMQIIQLQVLNKAKERQLENLIEKLNESERQIRY LNHQLVIIKDEKDGLTLSLRESQKLFQNGKEREIQ LEAQIKALETQIQALKVNEEQMIKKSRTTEMALE SLKQQLVDLHHSESLQRAREQHESIVMGLTKKY EEQVLSLQKNLDATVTALKEQEDICSRLKDHVK

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				QLERNQEAIKLEKTEIINKLTRSLEESQKQCAHLL QSGSVQEVAQLQFQLQQAQKAHAMSANMNKA LQEELTELKDEISLYESAAKLGIHPSDSEGELNIEL TESYVDLGIKKVNWKKSKVTSIVQEEDPNEELSK DEFILKLKAEVQRLLGSNSMKRHLVSQLQNDLK DCHKKIEDLHQVKKDEKSIEVETKTDTSEKPKNQ LWPESSTSDVVRDDILLLKNEIQVLQQQNQELKE TEGKLRNTNQDLCNQMRQMVQDFDHDKQEAV DRCERTYQQHHEAMKTQIRESLLAKHALEKQQL FEAYERTHLQLRSELDKLNKEVTAVQECYLEVC REKDNLELTLRKTTEKEQQTQEKIKEKLIQQLEK EWQSKLDQTIKAMKKKTLDCGSQTDQVTTSDVI SKKEMAIMIEEQKCTIQQNLEQEKDIAIKGAMKK LEIELELKHCENITKQVEIAVQNAHQRWLGELPE LAEYQALVKAEQKKWEEQHEVSVNKRISFAVSE AKEKWKSELENMRKNILPGKELEEKIHSLQKELE LKNEEVPVVIRAELAKARSEWNKEKQEEIHRIQE QNEQDYRQFLDDHRNKINEVLAAAKEDFMKQK TELLLQKETELQTCLDQSRREWTMQEAKRIQLEI YQYEEDILTVLGVLLSDTQKEHISDSEDKQLLEI MSTCSSKWMSVQYFEKLKGCIQKAFQDTLPLLV ENADPEWKKRNMAELSKDSASQGTGQGDPGPA AGHHAQPLALQATEAEADKKKVLEIKDLCCGHC FQELEKAKQECQDLKGKLEKCCRHLQHLERKHK AVVEKIGEENNKVVEELIEENNDMKNKLEELQT LCKTPPRSLSAGAIENACLPCSGGALEELRGQYIK AVKKIKCDMLRYIQESKERAAEMVKAEVL*ERQ ETARKMRKYYLICLQQILQDDGKEGAEKKIMNA ASKLATMAKLLETPISSKSQSKTTQSGMSK
3552	A	771	375	ARTRQTSGQAREPEKESPAPGGGGLAEIRSRQQL SQTSRIPPLAKDQAVEAMFPPARGKELLSFEDVA MYFTREEWGHLNWGQKDLYRDVMLENYRNMV LLVYFQFDAAIPLC*TSLAHSSWLQLYFRLYF
3553	A	76	72	PGVRGVEAPGGVAPGRNAMRRGERRDAGGPRP ESPVPAGRASLEEPPDGPSAGQATGPGEGRRSTE SEVYDDGTNTFFWRAHTLTVLFILTCTLGYVTLL EETPQDTAYNTKRGIVASILVFLCFGVTQAKDGP FSRPHPAYWRFWLCVSVVYELFLIFILFQTVQDG RQFLKYVDPKLGVPLPERDYGGNCLIYDPDNET DPFHNIWDKLDGFVPAHFLGWYLKTLMIRDWW MCMIISVMFEFLEYSLEHQLPNFSECWWDHWIM DVLVCNGLGIYCGMKTLEWLSLKTYKWQGLWN IPTYKGKMKRIAFQFTPYSWVRFEWKPASSLRR WLAVCGIILVFLLAELNTFYLKFVLWMPPEHYLV LLRLVFFVNVGGVAMREIYDFMDDPKPHKKLGP QAWLVAAITATELLIVVKYDPHTLTLSLPFYISQC WTLGSVLALTWTVWRFFLRDITLRYKETRWQK WQNKDDQGSTVGNGDQHPLGLDEDLLGPGVAE GEGAPTPN*PRGPAPRPLPSAPRAVCGASSRR
3554	A	2	2106	FDEFSALPSPSLQTSWSFGPMSRRALRRLRGEQR GQEPLGPGALHFDLRDDDDAEEEGPKRELGVRR PGGAGKEGVRVNNRFELINIDDLEDDPVVNGERS GCALTDAVAPGNKGRGQRGNTESKTDGDDTET VPSEQSHASGKLRKKKKKQKNKKSSTGEASENG LEDIDRILERIEDSTGLNRPGPAPLSSRKHVLYVE

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				HRHLNPDTELKRYFGARAILGEQRPRQRQRVYP KCTWLTTPKSTWPRYSKPGLSMRLLESKKGLSFF AFEHSEEYQQAQHKFLVAVESMEPNNIVVLLQT SPYHVDSLLQLSDACRFQEDQEMARDLVERALY SMECAFHPLFSLTSGACRLDYRRPENRSFYLALY KQMSFLEKRGCPRTALEYCKLILSLEPDEDPLCM LLLIDHLALRARNYEYLIRLFQEWEVGASLAHRN LSQLPNFAFSVPLAYFLLSQQTDLPECEQSSARQ KASLLIQQALTMFPGVLLPLLESCSVRPDASVSSH RFFGPNAEISQPPALSQLVNLYLGRSHFLWKEPA TMSWLEENVHEVLQAVDAGDPAVEACENRRKV LYQRAPRNIHRHVILSEIKEAVAALPPDVTTQSV MGFDPLPPSDTIYSYVRPERLSPISHGNTIALFFRS LLPNYTMEGERPEEGVAGGLNRNQGLNRLMLA VRDMMANFHLNDLEAPHEDDA*GEGEWD
3555	A	2	2106	FDEFSALPSPSLQTSWSFGPMSRRALRRLRGEQR GQEPLGPGALHFDLRDDDDAEEEGPKRELGVRR PGGAGKEGVRVNNRFELINIDDLEDDPVVNGERS GCALTDAVAPGNKGRGQRGNTESKTDGDDTET VPSEQSHASGKLRKKKKKQKNKKSSTGEASENG LEDIDRILERIEDSTGLNRPGPAPLSSRKHVLYVE HRHLNPDTELKRYFGARAILGEQRPRQRQRVYP KCTWLTTPKSTWPRYSKPGLSMRLLESKKGLSFF AFEHSEEYQQAQHKFLVAVESMEPNNIVVLLQT SPYHVDSLLQLSDACRFQEDQEMARDLVERALY SMECAFHPLFSLTSGACRLDYRRPENRSFYLALY KQMSFLEKRGCPRTALEYCKLILSLEPDEDPLCM LLLIDHLALRARNYEYLIRLFQEWEVGASLAHRN LSQLPNFAFSVPLAYFLLSQQTDLPECEQSSARQ KASLLIQQALTMFPGVLLPLLESCSVRPDASVSSH RFFGPNAEISQPPALSQLVNLYLGRSHFLWKEPA TMSWLEENVHEVLQAVDAGDPAVEACENRRKV LYQRAPRNIHRHVILSEIKEAVAALPPDVTTQSV MGFDPLPPSDTIYSYVRPERLSPISHGNTIALFFRS LLPNYTMEGERPEEGVAGGLNRNQGLNRLMLA VRDMMANFHLNDLEAPHEDDA*GEGEWD
3556	A	3388	1650	KTRGTMFYYPNVLQRHTGCFATIWLAATRGSRL VKREYLRVNVVKTCEEILNYVLVRVQPPQPGLP RPRFSLYLSAQLQIGVIRVYSQQCQYLVEDIQHIL ERLHRAQLQIRIDMETELPSLLLPNHLAMMETLE DAPDPFFGMMSVDPRLPSPFDIPQIRHLLEAAIPE RVEEIPPEVPTEPREPERIPVTVLPPEAITILEAEPIR MLEIEGERELPEVSRRELDLLIAEEEEAILLEIPRL PPPAPAE*GQELLDQVGCQCWEGSPHFSCPFPLR VEGMGEALGPEELRLTGWEPGALLMEVTPPEEL RLPAPPSPERRPPVPPPPRRRRRRRLLFWDKETQI SPEKFQEQLQTRAHCWECPMVQPPERTIRGPAEL FRTPTLSGWLPPELLGLWTHCAQPPPKALRRELP EEAAAEEERRKIEVPSEIEVPREALEPSVPLMVSL EISLEAAEEEKSRISLIPPEERWAWPEVEAPEAPA LPVVPELPEVPMEMPLVLPPELELLSLEAVHRAV ALELQANREPDFSSLVSPLSPRRMAARVFYLLLV LSAQQILHVKQEKPYGRLLIQPGPRFH
3557	A	3388	1650	KTRGTMFYYPNVLQRHTGCFATIWLAATRGSRL VKREYLRVNVVKTCEEILNYVLVRVQPPQPGLP

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				RPRFSLYLSAQLQIGVIRVYSQQCQYLVEDIQHIL ERLHRAQLQIRIDMETELPSLLLPNHLAMMETLE DAPDPFFGMMSVDPRLPSPFDIPQIRHLLEAAIPE RVEEIPPEVPTEPREPERIPVTVLPPEAITILEAEPIR MLEIEGERELPEVSRRELDLLIAEEEEAILLEIPRL PPPAPAE*GQELLDQVGCQCWEGSPHFSCPFPLR VEGMGEALGPEELRLTGWEPGALLMEVTPPEEL RLPAPPSPERRPPVPPPPRRRRRRRLLFWDKETQI SPEKFQEQLQTRAHCWECPMVQPPERTIRGPAEL FRTPTLSGWLPPELLGLWTHCAQPPPKALRRELP EEAAAEEERRKIEVPSEIEVPREALEPSVPLMVSL EISLEAAEEEKSRISLIPPEERWAWPEVEAPEAPA LPVVPELPEVPMEMPLVLPPELELLSLEAVHRAV ALELQANREPDFSSLVSPLSPRRMAARVFYLLLV LSAQQILHVKQEKPYGRLLIQPGPRFH
3558	A	489	2360	IRPRPRGRRRALDSPNAAAPPVYVCRSPGEPTSL VNMASEDIAKLAETLAKTQVAGGQLSFKGKSLK LNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEA ARVIAKAL*KKSELKRCHWSDMFTGRLRTEIPPA LISLGEGLITAGAQLVELDLSDNAFGPDGVQGFE ALLKSSACFTLQELKLNNCGMGIGGGKILAAALT ECHRKSSAQGKPLALKVFVAGRNRLENDGATAL AEAFRVIGTLEEVHMPQNGINHPGITALAQAFAV NPLLRVINLNDNTFTEKGAVAMAETLKTLRQVE VINFGDCLVRSKGAVAIADAIRGGLPKLKELNLS FCEIKRDAALAVAEAMADKAELEKLDLNGNTLG EEGCEQLQEVLEGFNMAKVLASLSDDEDEEEE EGEEEEEAEEEEEEDEEEEEEEEEEEEEEPQQRG QGEKSATPSRKILDPNTGEPAPVLSSPPPADVSTF LAFPSPEKLLRLGPKSSVLIAQQTDTSDPEKVVSA FLKVSSVFKDEATVRMAVQDAVDALMQKAFNS SSFNSNTFLTRLLVHMGLLKSEDKVKAIANLYGP LMALNHMVQQDYFPKALAPLLLAFVTKPNSALE SCSFARHSLLQTLYKV
3559	A	489	2360	IRPRPRGRRRALDSPNAAAPPVYVCRSPGEPTSL VNMASEDIAKLAETLAKTQVAGGQLSFKGKSLK LNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEA ARVIAKAL*KKSELKRCHWSDMFTGRLRTEIPPA LISLGEGLITAGAQLVELDLSDNAFGPDGVQGFE ALLKSSACFTLQELKLNNCGMGIGGGKILAAALT ECHRKSSAQGKPLALKVFVAGRNRLENDGATAL AEAFRVIGTLEEVHMPQNGINHPGITALAQAFAV NPLLRVINLNDNTFTEKGAVAMAETLKTLRQVE VINFGDCLVRSKGAVAIADAIRGGLPKLKELNLS FCEIKRDAALAVAEAMADKAELEKLDLNGNTLG EEGCEQLQEVLEGFNMAKVLASLSDDEDEEEE EGEEEEEAEEEEEEDEEEEEEEEEEEEEEPQQRG QGEKSATPSRKILDPNTGEPAPVLSSPPPADVSTF LAFPSPEKLLRLGPKSSVLIAQQTDTSDPEKVVSA FLKVSSVFKDEATVRMAVQDAVDALMQKAFNS SSFNSNTFLTRLLVHMGLLKSEDKVKAIANLYGP LMALNHMVQQDYFPKALAPLLLAFVTKPNSALE SCSFARHSLLQTLYKV
3560	A	2	1198	FVRELPRPRPGAATAAIMVSVINTVDTSHEDMIH DAQMDYYGTRLATCSSDRSVKIFDVRNGGQILIA

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				DLRGHEGPVWQVAWAHPMYGNILASCSYDRKV IIWREENGTWEKSHEHAGHDSSVNSVCWAPHDY GLILACGSSDGAISLLTYTGEGQWEVKKINNAHT IGCNAVSWAPAVVPGSLIDHPSGQKPNYIKRFAS GGCDNLIKLWKEEEDGQWKEEQKLEAHSDWVR DVAWAPSIGLPTSTIASCSQDGRVFIWTCDDASS NTWSPKLLHKFNDVVWHVSWSITANILAVSGGD NKVTLWKESVDGQWVCISDVNKGQGSVSASVT EGQQNEQ*QDRWGLAPHPPAPGLPLPGPTNQTT GKSPQLQQDYFPRRSYRCSHRLIICLNVIGDAL
3561	A	540	86	WRVKEMTSTLPKALGRKTASRSHTTLQGGSCCP VLWTAKLRCRKLRFPLPPPPPSSSAWPWQGWGI RGEQEAEGPLGETGPPVGPELSGLRQWRKLIKGR YGEWRGSGQKTGQPS*TTMQGGETEENRTETTT GNKQRESEAPWVRHTYIT
3562	A	1920	242	PMMAMPFFERFKSSIQRPSPVLVLSQNTKRESGR KVQSGNINAAKTIADIIRTCLGPKSMMKMLLDP MGGIVMTNDGNAILREIQVQHPAAKSMIEISRTQ DEEVGDGTTSVIILAGEMLSVAEHFLEQQMHPTV VISAYRKALDDMISTLKKISIPVDISDSDMMLNIIN SSITTKAISRWSSLACNIALDAVKMVQFEENGRK EIDIKKYARVEKIPGGIIEDSCVLRGVMINKDVTH PRMRRYIKNPRIVLLDSSLEYKKGESQTDIEITRE EDFTRILQMEEEYIQQLCEDIIQLKPDVVITEKGIS DLAQHYLMRANITAIRRVRKTDNNRIARACGARI VSRPEELREDDVGTGAGLLEIKKIGDEYFTFITDC KDPKACTILLRGASKEILSEVERNFQDAMQVCRN VLLDPQLVPGGGASEMAVAHALTEKSKAMTGV EQWPYRAVAQALEVIPRTLIQNCGASTIRLLTSLR AKHTQENCETWGVNGETGTLVDMKELGIWEPL AVKLQTYKTAVETAVLLLRIDDIVSGHKKKGDD QSRQGGAPDAGQE
3563	A	1571	560	GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAV DDLQFEEFGNAATSLTANPDATTVNIEDPGETPK HQPGSPRGSGREEDDELLGNDDSDKTELLAGQK KSSPFWTFEYYQTFFDVDTYQVFDRIKGSLLPIPG KNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLS NFLIHLGEKTYHYVPEFRKVSIAATIIYAYAWLVP LALWGFLMWRNSKVMNIVSYSFLEIVCVYGYSL FIYIPTAILWIIPHKAVRWILVMIALGISGSLLAMT FWPAVREDNRRVALATIVTIVLLHMLLSVGCLA YFFDAPEMDHLPTTTATPNQTVAAAKSS
3564	A	1	328	NSRVDDFVAHLQRPLLGPASCLGILRPAMTAHSF ALPGIIFTTFWGLVGIAGPWFVPKGPNRGVIITML VATAVCCYLFWLIAILAQLNPLFGPQLKNETIWY VRFLWE
3565	A	2	1081	FVTDFPARSMAATSLMSALAARLLQPAHSCSLRL RPFHLAAVRNEAVVISGRKLAQQIKQEVRQEVEE WVASGNKRPHLSVILVGENPASHSYVLNKTRAA AVVGINSETIMKPASISEEELLNLINKLNNDDNVD GLLVQLPLPEHIDERRICNAVSPDKDVDGFHVIN VGRMCLDQYSMLPATPWGVWEIIKRTGIPTLGK NVVVAGRSKNVGMPIAMLLHTDGAHERPGGDA TVTISHRYTPKEQLKKHTILADIVISAAGIPNLITA DMIKEGAAVIDVGINRVHDPVTAKPKLVGDVDF

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				EGVRQKAGYITPVPGGVGPMTVAMLMKNTIIAA KKVLRLEEREVLKSKELGVATN
3566	A	3	1130	SCRRGRQQQRRNVSLSSQFAHTMAAPAQQTTQP GGGKRKGKAQYVLAKRARRCDAGGPRQLEPGL QGILITCNMNERKCVEEAYSLLNEYGDDMYGPE KFTDKDQQPSGSEGEDDDAEAALKKEVGDIKAS TEMRLRRFQSVESGANNVVFIRTLGIEPEKLVHHI LQDMYKTKKKKTRVILRMLPISGTCKAFLEDMK KYAETFLEPWFKAPNKGTFQIVYKSRNNSHVNR EEVIRELAGIVCTLNSENKVDLTNPQYTVVVEIIK AVCCLSVVKDYMLFRKYNLQEVVKSPKDPSQLN SKQGNGKEAKLESADKSDQNNTAEGKNNQQVP ENTEELGQTKPTSNPQVVNEGGAKPELASQATE GSKSNENDFS
3567	A	248	3498	GKKDSSPWTCPFHPPLQLFFVIRNTRQLGDFHLA KIKVRNYWTADGDLDIGAKNVKLYVNRNLIFNG KLDKGDREAPADHSILVDQKNEKSEQLEEAMNA HSEESKGTHEMAGASGDKELGLGCSPPAETLAD AKLSSQGNVSGKRKNSTNCRKDSLSQLEEYLRLS AVPTSMGDMPSAPATSPPVKCPPVHEEPSLIQQL ENLMGRKICEPPGKTPSWLQPSPTGKDRKQGGR KPKPLWLSPEKPLAWKGRLPSDDVIGEGPGETEA RDKGLRHEPGWGTSRSVNTKERPQRATTKVHSD DSDIFNQPPNRERPASGRRGSRKDAGSSSHGDDQ PASREDTWSSRTPSRSRWRSEQEHTLHESWSSLS AFDRSHRGRISNTELPGDILDELLQQKSSRHSDLP PSKKGEQPGLSRGQDGYSGETDAGGDFKIPVLPY GQRLVIDIKSTWGDRHYVGLNGIEIFSSKGEPVQI SNIKADPPDINILPAYGKDPRVVTNLIDGVNRTQ DDMHVWLAPFTRGRSHSITIDFTHPCHVALIRIW NYNKSRIHSFRGVKDITMLLDTQCIFEGEIAKASG TLAGAPEHFGDTILFTTDDDILEAIFYSDEMFDLD VGSLDSLQDEEAMRRPSTADGEGDERPFTQAGL GADERIPELELPSSSPVPQVTTPEPGIYHGICLQLN FTASWGDLHYLGLTGLEVVGKEGQALPIHLHQIS ASPRDLNELPEYSDDSRTLDKLIDGTNITMEDEH MWLIPFSPGLDHVVTIRLDRAESIAGLRFWNYNK SPEDTYRGAKIVHVSLDGLCVSPPEGFLIRKGPG NCHFDFAQEILFVDYLRAQLLPQPARRLDMRSLE CASMDYEAPLMPCGFIFQFQLLTSWGDPYYIGLT GLELYDERGEKIPLSENNIAAFPDSVNSLEGVGG DVRTPDKLIDQVNDTSDGRHMWLAPILPGLVNR VYVIFDLPTTVSMIKLWNYAKTPHRGVKEFGLL VDDLLVYNGILAMVSHLVGGILPTCEPTVPYHTI LFTEDRDIRHQEKHTTISNQAEDQDVQMMNENQ IITNAKRKQSVVDPALRPKTCISEKETRRRRC
3568	A	50	1724	AQGGTLSAASRFCRGGLLGPWLHPASEMAATLD LKSKEEKDAELDKRIEALRRKNEALIRRYQEIEE DRKKAELEGVAVTAPRKGRSVEKENVAVESEKN LGPSRRSPGTPRPPGASKGGRTPPQQGGRAGMG RASRSWEGSPGEQPRGGGAGGRGRRGRGRGSPH LSGAGDTSISDRKSKEWEERRRQNIEKMNEEME KIAEYERNQREGVLEPNPVRNFLDDPRRRSGPLE ESERDRREESRRHGRNWGGPDFERVRCGLEHER QGRRAGLGSAGDMTLSMTGRERSEYLRWKQER

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				EKIDQERLQRHRKPTGQWRREWDAEKTDGMFK DGPVPAHEPSHRYDDQAWARPPKPPTFGEFLSQ HKAEASSRRRRKSSRPQAKAAPRAYSDHDDRWE TKEGAASPAPETPQPTSPETSPKETPMQPPEIPAP AHRPPEDEGEENEGEEDEEWEDISEDEEEEEIEVE EGDEEEPAQDHQAPEAAPTGIPCSEQAHGVPFSP EEPLLEPQAPGTPSSPFSPPSGHQPVSDWGEEVEL NSPRTTHLAGALSPGEAWPFESV
3569	A	1	912	MGRVGRAGVQLGRRRTTWAAERTGQAAAGGP GRALRGQRPDLRSGGAADSPAAGRGELYCGVLP RSPWFLSERRRQMADFDTYDDRAYSSFGGGRGS RGSAGGHGSRSQKELPTEPPYTAYVGNLPFNTV QGDIDAIFKDLSIRSVRLVRDKDTDKFKGFCYVE FDEVDSLKEALTYDGALLGDRSLRVDIAEGRKQ DKGGFGFRKGGPDDRGFRDDFLGGRGGSRPGDR RTGPPMGSRFRDGPPLRGSNMDFREPTEEERAQR PRLQLKPRTVATPLNQVANPNSAIFGGARPREEV VQKEQE
3570	A	1	912	MGRVGRAGVQLGRRRTTWAAERTGQAAAGGP GRALRGQRPDLRSGGAADSPAAGRGELYCGVLP RSPWFLSERRRQMADFDTYDDRAYSSFGGGRGS RGSAGGHGSRSQKELPTEPPYTAYVGNLPFNTV QGDIDAIFKDLSIRSVRLVRDKDTDKFKGFCYVE FDEVDSLKEALTYDGALLGDRSLRVDIAEGRKQ DKGGFGFRKGGPDDRGFRDDFLGGRGGSRPGDR RTGPPMGSRFRDGPPLRGSNMDFREPTEEERAQR PRLQLKPRTVATPLNQVANPNSAIFGGARPREEV VQKEQE
3571	A	28	131	RHFFGNLCAMRAKWRKKRMRRLKRKRRKMRQ RSK
3572	A	3	1202	QSEPHRKVRVDPPVRDRPPPHPPPLLVQRALPGQ GQAEGSDGADGAKRRAMAHQTGIHATEELKEFF AKARAGSVRLIKVVIEDEQLVLGASQEPVGRWD QDYDRAVLPLLDAQQPCYLLYRLDSQNAQGFE WLFLAWSPDNSPVRLKMLYAATRATVKKEFGG GHIKDELFGTVKDDLSFAGYQKHLSSCAAPAPLT SAERELQQIRINEVKTEISVESKHQTLQGLAFPLQ PEAQRALQQLKQKMVNYIQMKLDLERETIELVH TEPTDVAQLPSRVPRDAARYHFFLYKHTHEGDP LESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSV EQDFHLEIAKKIEIGDGAELTAEFLYDEVHPKQH AFKQAFAKPKGPGGKRGHKRLIRGPGENGDDS
3573	A	49	1869	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEV EEISLLQPQVEESVLNLGKFHSIVRLVAFCPFASS QVALENANAVSEGVVHEDLRLLLETHLPSKKKK VLLGVGDPKIGAAIQEELGYNCQTGGVIAEILRG VRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKV KFNVNRVDNMIIQSISLLDQLDKDINTFSMRVRE WYGYHFPELVKIINDNATYCRLAQFIGNRRELNE DKLEKLEELTMDGAKAKAILDASRSSMGMDISAI DLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAP SLSALIGEAVGARLIAHAGSLTNLAKYPASTVQIL GAEKALFRALKTRGNTPKYGLIFHSTFIGRAAAK NKGRISRYLANKCSIASRIDCFSEVPTSVFGEKLR EQVEERLSFYETGEIPRKNLDVMKEAMVQAEAE

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				EAAAEITRKLEKQEKKRLKKEKKRLAALALASS ENSSSTPEECEETSEKPKKKKKQKPQEVPQENGM EDPSISFSKPKKKKSFSKEELMSSDLEETAGSTSIP KRKKSTPKEETVNDPEEAGHRSRSKKKRKFSKEE PVSSGPEEAVGKSSSKKKKKKFHKASQED
3574	A	284	2032	CGNERTARLWVQPVVSTMPQASEHRLGRTREPP VNIQPRVGSKLPFAPRARSKERRNPASGPNPMLR PLPPRPGLPDERLKKLELGRGRTSGPRPRGPLRA DHGVPLPGSPPPTVALPLPSRTNLARSKSVSSGDL RPMGIALGGHRGTGELGAALSRLALRPEPPTLRR STSLRRLGGFPGPPTLFSIRTEPPASHGSFHMISAR SSEPFYSDDKMAHHTLLLGSGHVGLRNLGNTCF LNAVLQCLSSTRPLRDFCLRRDFRQEVPGGGRA QELTEAFADVIGALWHPDSCEAVNPTRFRAVFQ KYVPSFSGYSQQDAQEFLKLLMERLHLEINRRGR RAPPILANGPVPSPPRRGGALLEEPELSDDDRANL MWKRYLEREDSKIVDLFVGQLKSCLKCQACGY RSTTFEVFCDLSLPIPKKGFAGGKVSLRDCFNLFT KEEELESENAPVCDRCRQKTRSTKKLTVQRFPRI LVLHLNRFSASRGSIKKSSVGVDFPLQRLSLGDF ASDKAGSPVYQLYALCNHSGSVHYGHYTALCR CQTGWHVYNDSRVSPVSENQVASSEGYVLFYQL MQEPPRCL
3575	A	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVK LIISEGRPTIEVRRCSMPSVICEHTKQFQTISEESN QGSLLTVPGDTSPSPKPEVFSNVPERDLSNVSNIH SSFATSPTGASNSKYVSADRNLIKNTAPVNTVMD SPVHLEPSSQVGVIQNKSWEMPVDRLETLSTRDF ICPNSNIPDQESSLQSFCNSENKVLKENADFLSLR QTELPGNSCAQDPASFMPPQQPCSFPSQSLSDAES ISKHMSLSYVANQEPGILQQKNAVQIISSALDTD NESTKDTENTFVLGDVQKTDAFVPVYSDSTIQEA SPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAF SKLTYKSSSGHEVENSTTDTQVISHEKENKLESL VLTHLSRCDSDLCEMNAGMPKGNLNEQDPKHC PESEKCLLSIEDEESQQSILSSLENHSQQSTQPEM HKYGQLVKVELEENAEDDKTENQIPQRMTRNK ANTMANQSKQILASCTLLSEKDSESSSPRGRIRLT EDDDPQIHHPRKRKVSRVPQPVQVSPSLLQAKEK TQQSLAAIVDSLKLDEIQPYSSERANPYFEYLHIR KKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLLD GNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKL RLQHSIEREKLIVSNEQEVLRVHYRAARTLANQT LPFSACTVLLDAEVYNVPLDSQSDDSKTSVRDRF NARQFMSWLQDVDDKFDKLKTCLLMRQQHEA AALNAVQRLEWQLKLQELDPATYKSISIYEIQEF YVPLVDVNDDFELTPI
3576	A	5	1421	LRLAWHDGARWPLGTPRAAATRREAAALPPVT LALLCLDGVFLSSAENDFVHRIQEELDRFLLQKQ LSKVLLFPPLSSRLRYLIHRTAENFDLLSSFSVGE GWKRRTVICHQDIRVPSSDGLSGPCRAPASCPSR YHGPRPISNQGAAAVPRGARAGRWYRGRKPDQ PLYVPRVLRRQEEWGLTSTSVLKREAPAGRDPEE PGDVGAGDPNSDQGLPVLMTQGTEDLKGPGQR CENEPLLDPVGPEPLGPESQSGKGDMVEMATRF

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				GSTLQLDLEKGKESLLEKRLVAEEEEDEEEVEED GPSSCSEDDYSELLQEITDNLTKKEIQIEKIHLDTS SFMEELPGEKDLAHVVEIYDFEPALKTEDLLATF SEFQEKGFRIQWVDDTHALGIFPCRASAAEALTR EFSVLKIRPLTQGTKQSKLKALQRPKLLRLVKER PQTNATVARRLVARALGLQHKKKERPAVRGPLP P
3577	A	102	1998	DTRTPGSLEMGPLQFRDVAIEFSLEEWHCLDTAQ RNLYRNVMLENYSNLVFLGIVVSKPDLIAHLEQG KKPLTMKRHEMVANPSGPVICSHFAQDLWPEQN IKDSFQKVILRRYEKRGHGNLQLIKRCESVDECK VHTGGYNGLNQCSTTTQSKVFQCDKYGKVFHK FSNSNRHNIRHTEKKPFKCIECGKAFNQFSTLITH KKIHTGEKPYICEECGKAFKYSSALNTHKRIHTG EKPYKCDKCDKAFIASSTLSKHEIIHTGKKPYKCE EECGKAFNQSSTLTKHKKIHTGEKPYKCEECGKAF NQSSTLTKHKKIHTGEKPYVCEECGKAFKYSRIL TTHKRIHTGEKPYKCNKCGKAFIASSTLSRHEFIH MGKKHYKCEECGKAFIWSSVLTRHKRVHTGEKP YKCEECGKAFKYSSTLSSHKRSHTGEKPYKCEEC GKAFVASSTLSKHEIIHTGKKPYKCEECGKAFNQ SSSLTKHKKIHTGEKPYKCEECGKAFNQSSSLTK HKKIHTGEKPYKCEECGKAFNQSSTLIKHKKIHT REKPYKCEECGKAFHLSTHLTTHKILHTGEKPYR CRECGKAFNHSATLSSHKKIHSGEKPYECDKCG KAFISPSSLSRHEIIHTGEKP
3578	A	1725	445	RPRRRGTHHFSCVLGSFRVSAMFPRVSTFLPLRP LSRHPLSSGSPETSAAAIMLLTVRHGTVRYRSSA LLARTKNNIQRYFGTNSVICSKKDKQSVRTEETS KETSESQDSEKENTKKDLLGIIKGMKVELSTVNV RTTKPPKRRPLKSLEATLGRLRRATEYAPKKRIEP LSPELVAAASAVADSLPFDKQTTKSELLSQLQQH EEESRAQRDAKRPKISFSNIISDMKVARSATARV RSRPELRIQFDEGYDNYPGQEKTDDLKKRKNIFT GKRLNIFDMMAVTKEAPETDTSPSLWDVEFAKQ LATVNEQPLQNGFEELIQWTKEGKLWEFPINNEA GFDDDGSEFHEHIFLEKHLESFPKQGPIRHFMELV TCGLSKNPYLSVKQKVEHIEWFRNYFNEKKDILK ESNIQFKLRPWKFLFRNN
3579	A	1725	445	RPRRRGTHHFSCVLGSFRVSAMFPRVSTFLPLRP LSRHPLSSGSPETSAAAIMLLTVRHGTVRYRSSA LLARTKNNIQRYFGTNSVICSKKDKQSVRTEETS KETSESQDSEKENTKKDLLGIIKGMKVELSTVNV RTTKPPKRRPLKSLEATLGRLRRATEYAPKKRIEP LSPELVAAASAVADSLPFDKQTTKSELLSQLQQH EEESRAQRDAKRPKISFSNIISDMKVARSATARV RSRPELRIQFDEGYDNYPGQEKTDDLKKRKNIFT GKRLNIFDMMAVTKEAPETDTSPSLWDVEFAKQ LATVNEQPLQNGFEELIQWTKEGKLWEFPINNEA GFDDDGSEFHEHIFLEKHLESFPKQGPIRHFMELV TCGLSKNPYLSVKQKVEHIEWFRNYFNEKKDILK ESNIQFKLRPWKFLFRNN
3580	A	3673	1619	LYCVAPYSRHLLGRMSHLPMKLLRKKIEKRNLK LRQRNLKFQGASNLTLSETQNGDVSEETMGSRK VKKSKQKPMNVGLSETQNGGMSQEAVGNIKVT

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				KSPQKSTVLTNGEAAMQSSNSESKKKKKKKRK MVNDAEPDTKKAKTENKGKSEEESAETTKETEN NVEKPDNDEDESEVPSLPLGLTGAFEDTSFASLC NLVNENTLKAIKEMGFTNMTEIQHKSIRPLLEGR DLLAAAKTGSGKTLAFLIPAVELIVKLRFMPRNG TGVLILSPTRELAMQTFGVLKELMTHHVHTYGLI MGGSNRSAEAQKLGNGINIIVATPGRLLDHMQN TPGFMYKNLQCLVIDEADRILDVGFEEELKQIIKL LPTRRQTMLFSATQTRKVEDLARISLKKEPLYVG VDDDKANATVDGLEQGYVVCPSEKRFLLLFTFL KKNRKKKLMVFFSSCMSVKYHYELLNYIDLPVL AIHGKQKQNKRTTTFFQFCNADSGTLLCTDVAA RGLDIPEVDWIVQYDPPDDPKEYIHRVGRTARGL NGRGHALLILRPEELGFLRYLKQSKVPLSEFDFS WSKISDIQSQLEKLIEKNYFLHKSAQEAYKSYIRA YDSHSLKQIFNVNNLNLPQVALSFGFKVPPFVDL NVNSNEGKQKKRGGGGGFGYQKTKKVEKSKIF KHISKKSSDSRQFSH
3581	A	23	453	LCRCICIKNITPHCLWDKVLSQFTYILDNLSNFMS HHPHSLRNSCLIRMDLLYWQFTIYTITFCFSHLSG RLTLSAQHISHRPCLLSYSLLFWKVHHLFLEGFPC SPRLDEMSFHQFPQHPVHVSVVHLPIVYKGSMT QVSPH
3582	A	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEA GIEAVGSAAEEKGGLVSDAYGEDDFSRLGGDED GYEEEEDENSRQSEDDDSETEKPEADDPKDNTE AEKRDPQELVASFSERVRNMSPDEIKIPPEPPGRC SNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRN PSIYEKLIQFCAIDELGTNYPKDMFDPHGWSEDS YYEALAKAQKIEMDKLEKAKKERTKIEFVTGTK KGTTTNATSTTTTTASTAVADAQKRKSKWDSAI PVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVIS AVGTIVKKAKQ
3583	A	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEA GIEAVGSAAEEKGGLVSDAYGEDDFSRLGGDED GYEEEEDENSRQSEDDDSETEKPEADDPKDNTE AEKRDPQELVASFSERVRNMSPDEIKIPPEPPGRC SNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRN PSIYEKLIQFCAIDELGTNYPKDMFDPHGWSEDS YYEALAKAQKIEMDKLEKAKKERTKIEFVTGTK KGTTTNATSTTTTTASTAVADAQKRKSKWDSAI PVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVIS AVGTIVKKAKQ
3584	A	3	1139	PGSTISSRADRLGAPVLAHPKMAERQEEQRGSPP LRAEGKADAEVKLILYHWTHSFSSQKVRLVIAE KALKCEEHDVSLPLSEHNEPWFMRLNSTGEVPV LIHGENIICEATQIIDYLEQTFLDERTPRLMPDKES MYYPRVQHYRELLDSLPMDAYTHGCILHPELTV DSMIPAYATTRIRSQIGNTESELKKLAEENPDLQE AYIAKQKRLKSKLLDHDNVKYLKKILDELEKVL DQVETELPRRNEETPEEGQQPWLCGESFTLADVS LAVTLHRLKFLGFARRNWGNGKRPNLETYYERV LKRKTFNKVLGHVNNILISAVLPTAFRVAKKRAP KVLGTTLVVGLLAGVGYFAFMLFRKRLGSMILA LRPRPNYF

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3585	A	1	1777	RRHSPGSPAFAPSSRATAICPRAARAPATLLLALG AVLWPAAGAWELTILHTNDVHSRLEQTSEDSSK CVNASRCMGGVARLFTKVQQIRRAEPNVLLLDA GDQYQGTIWFTVYKGAEVAHFMNALRYDAMA LGNHEFDNGVEGLIEPLLKEAKFPILSANIKAKGP LASQISGLYLPYKVLPVGDEVVGIVGYTSKETPF LSNPGTNLVFEDEITALQPEVDKLKTLNVNKIIAL GHSGFEMDKLIAQKVRGVDVVVGGHSNTFLYT GNPPSKEVPAGKYPFIVTSDDGRKVPVVQAYAF GKYLGYLKIEFDERGNVISSHGNPILLNSSIPEDPS IKADINKWRIKLDNYSTQELGKTIVYLDGSSQSC RFRECNMGNLICDAMINNNLRHTDEMFWNHVS MCILNGGGIRSPIDERNNGTITWENLAAVLPFGG TFDLVQLKGSTLKKAFEHSVHRYGQSTGEFLQV GGIHVVYDLSRKPGDRVVKLDVLCTKCRVPSYD PLKMDEVYKVILPNFLANGGDGFQMIKDELLRH DSGDQDINVVSTYISKMKVIYPAVEGRIKFSTGS HCHGSFSLIFLSLWAVIFVLYQ
3586	A	1399	881	LSNKDVLSPQLKDENSKLRRKLNEVQSFSEAQTE MVRTLERKLEAKMIKEESDYHDLESVVQQVEQN LELMTKRAVKAENHVVKLKQEISLLQAQVSNFQ RENEALRCGQGASLTVVKQNADVALQNLRVVM NSAQASIEQLVSGAETLNLVAEILKSIDRISEVKD EEEDS
3587	A	88	1639	GCVGRGLPLPPRHPTPPSSSSSPFVLLAFLLLVRL DPAVSGKMAAPRPPPARLSGVMVPAPIQDLEAL RALTALFKEQRNRETAPRTIFQRVLDILKKSSHA VELACRDPSQVENLASSLQLITECFRCLRNACIEC SVNQNSIRNLDTIGVAVDLILLFRELRVEQESLLT AFRCGLQFLGNIASRNEDSQSIVWVHAFPELFLS CLNHPDKKIVAYSSMILFTSLNHERMKELEENLN IAIDVIDAYQKHPESEWPFLIITDLFLKSPELVQA MFPKLNNQERVTLLDLMIAKITSDEPLTKDDIPVF LRHAELIASTFVDQCKTVLKLASEEPPDDEEALA TIRLLDVLCEMTVNTELLGYLQVFPGLLERVIDL LRVIHVAGKETTNIFSNCGCVRAEGDISNVANGF KSHLIRLIGNLCYKNKDNQDKVNELDGIPLILDN CNISDSNPFLTQWVIYAIRNLTEDNSQNQDLIAK MEEQGLADASLLKKVGFEVEKKGEKLILKSTRD TPKP
3588	A	3	1462	DSPRNRFEILGRPTRTPTRPGPRPAMEDLDALLSD LETTTSHMPRSGAPKERPAEPLTPPPSYGHQPQT GSGESSGASGDKDHLYSTVCKPRSPKPAAPAAPP FSSSSGVLGTGLCELDRLLQELNATQFNITDEIMS QFPSSKVASGEQKEDQSEDKKRPSLPSSPSPGLPK ASATSATLELDRLMASLSDFRVQNHLPASGPTQP PVVSSTNEGSPSPPEPTGKGSLDTMLGLLQSDLSR RGVPTQAKGLCGSCNKPIAGQVVTALGRAWHPE HFVCGGCSTALGGSSFFEKDGAPFCPECYFERFSP RCGFCNQPIRHKMVTALGTHWHPEHFCCVSCGE PFGDEGFHEREGRPYCRRDFLQLFAPRCQGCQGP ILDNYISALSALWHPDCFVCRECFAPFSGGSFFEH EGRPLCENHFHARRGSLCATCGLPVTGRCVSAL GRRFHPDHFTCTFCLRPLTKGSFQERAGKPYCQP CFLKLFG

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3589	A	226	6793	SPPKKSRKCNLSFRLISAERWRFFLLILMEMPRKP RLTLFVQRRIENIATEREFDPEEFYYLLEAAEGHA KEGQGIKTDIPRYIISQLGLNKDPLEEMAHLGNY DSGTAETPETDESVSSSNASLKLRRKPRESDFETI KLISNGAYGAVYFVRHKESRQRFAMKKINKQNL ILRNQIQQAFVERDILTFAENPFVVSMYCSFETRR HLCMVMEYVEGGDCATLMKNMGPLPVDMARM YFAETVLALEYLHNYGIVHRDLKPDNLLVTSMG HIKLTDFGLSKVGLMSMTTNLYEGHIEKDAREFL DKQVCGTPEYIAPEVILRQGYGKPVDWWAMGII LYEFLVGCVPFFGDTPEELFGQVISDEINWPEKDE APPPDAQDLITLLLRQNPLERLGTGGAYEVKQHR FFRSLDWNSLLRQKAEFIPQLESEDDTSYFDTRSE KYHHMETEEEDDTNDEDFNVEIRQFSSCSHRFSK VFSSIDRITQNSAEEKEDSVDKTKSTTLPSTETLS WSSEYSEMQQLSTSNSSDTESNRHKLSSGLLPKL AISTEGEQDEAASCPGDPHEEPGKPALPPEECAQ EEPEVTTPASTISSSTLSVGSFSEHLDQINGRSECV DSTDNSSKPSSEPASHMARQRLESTEKKKISGKV TKSLSASALSLMIPGDMFAVSPLGSPMSPHSLSSD PSSSRDSSPSRDSSAASASPHQPIVIHSSGKNYGFT IRAIRVYVGDSDIYTVHHIVWNVEEGSPACQAGL KAGDLITHINGEPVHGLVHTEVIELLLKSGNKVSI TTTPFENTSIKTGPARRNSYKSRMVRRSKKSKKK ESLERRRSLFKKLAKQPSPLLHTSRSFSCLNRSLS SGESLPGSPTHSLSPRSPTPSYRSTPDFPSGTNSSQ SSSPSSSAPNSPAGSGHIRPSTLHGLAPKLGGQRY RSGRRKSAGNIPLSPLARTPSPTPQPTSPQRSPSPL LGHSLGNSKIAQAFPSKMHSPPTIVRHIVRPKSAE PPRSPLLKRVQSEEKLSPSYGSDKKHLCSRKHSL EVTQEEVQREQSQREAPLQSLDENVCDVPPLSRA RPVEQGCLKRPVSRKVGRQESVDDLDRDKLKAK VVVKKADGFPEKQESHQKFHGPGSDLENFALFK LEEREKKVYPKAVERSSTFENKASMQEAPPLGSL LKDALHKQASVRASEGAMSDGPVPAEHRQGGG DFRRAPAPGTLQDGLCHSLDRGISGKGEGTEKSS QAKELLRCEKLDSKLANIDYLRKKMSLEDKEDN LCPVLKPKMTAGSHECLPGNPVRPTGGQQEPPPA SESRAFVSSTHAAQMSAVSFVPLKALTGRVDSGT EKPGLVAPESPVRKSPSEYKLEGRSVSCLEPIEGT LDIALLSGPQASKTELPSPESAQSPSPSGDVRASV PPVLPSSSGKKNDTTSARELSPSSLKMNKSYLLEP WFLPPSRGLQNSPAVSLPDPEFKRDRKGPHPTAR SPGTVMESNPQQREGSSPKHQDHTTDPKLLTCLG QNLHSPDLARPRCPLPPEASPSREKPGLRESSERG PPTARSERSAARADTCREPSMELCFPETAKTSDN SKNLLSVGRTHPDFYTQTQAMEKAWAPGGKTN HKDGPGEARPPPRDNSSLHSAGIPCEKELGKVRR GVEPKPEALLARRSLQPPGIESEKSEKLSSFPSLQ KDGAKEPERKEQPLQRHPSSIPPPPLTAKDLSSPA ARQHCSSPSHASGREPGAKPSTAEPSSSPQDPPKP VAAHSESSSHKPRPGPDPGPPKTKHPDRSLSSQK PSVGATKGKEPATQSLGGSSREGKGHSKSGPDVF PATPGSQNKASDGIGQGEGGPSVPLHTDRAPLDA KPQPTSGGRPLEVLEKPVHLPRPGHPGPSEPADQ

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				KLSAVGEKQTLSPKHPKPSTVKDCPTLCKQTDN RQTDKSPSQPAANTDRRAEGKKCTEALYAPAEG DKLEAGLSFVHSENRLKGAERPAAGVGKGFPEA RGKGPGPQKPPTEADKPNGMKRSPSATGQSSFRS TALPEKSLSCSSSFPETRAGVREASAASSDTSSAK AAGGMLELPAPSNRDHRKAQPAGEGRTHMTKS DSLPSFRVSTLPLESHHPDPNTMGGASHRDRALS VTATVGETKGKDPAPAQPPPARKQNVGRDVTKP SPAPNTDRPISLSNEKDFVVRQRRGKESLRSSPHK KAL
3590	A	3	935	RATTRPKNEVQDYVSVEYLSPHMGGTDPFKYSY PPLVDDDFQTPLCENGPITSEDETSSKEDIESDGK ETLETISNEEQTPLLKKINPTESTSKAEENEKVDS KVKAFKKPLSVFKGPLLHISPAEELYFGSTESGEK KTLIVLTNVTKNIVAFKVRTTAPEKYRVKPSNSS CDPGASVDIVVSPHGGLTVSAQDRFLIMAAEME QSSGTGPAELTQFWKEVPRNKVMEHRLRCHTVE SSKPNTLTLKDNAFNMSDKTSEDICLQLSRLLES NRKLEDQVQRCIWFQQLLLSLTMLLLAFVTSFFY LLYS
3591	A	303	2	GGSWGPLCPVSPAMSLSDPGLGYHPTCWTLRWP PLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCS CEAGGSCACAGSCKCKKCKCTSCKKSCCSCCPL
3592	A	1052	1779	GKTMMRKMLLAAALSVTAMTAHADYQCSVTP RDDVIVSPQTVQVKGENGNLVITPDGNVMYNGK QYSLNAAQREQAKDYQAELRSTLPWIDEGAKSR VEKARIALDKIIVQEMGESSKMRSRLTKLDAQVK EQMNRIIETRSDGLTFHYKAIDQVRAEGQQLVNQ AMGGILQDSINEMGAKAVLKSGGNPLQNVLGSL GGLQSSIQTEWKKQEKDFQQFGKDVCSRVVTLE DSRKALVGNLK
3593	A	3	1837	LSFEKVDIQTDNDLTKEMYEGKENVSFELQRDFS QETDFSEASLLEKQQEVHSAGNIKKEKSNTIDGT VKDETSPVEECFFSQSSNSYQCHTITGEQPSGCTG LGKSISFDTKLVKHEIINSEERPFKCEELVEPFRCD SQLIQHQENNTEEKPYQCSECGKAFSINEKLIWH QRLHSGEKPFKCVECGKSFSYSSHYITHQTIHSGE KPYQCKMCGKAFSVNGSLSRHQRIHTGEKPYQC KECGNGFSCSSAYITHQRVHTGEKPYECNDCGK AFNGNAKLIQHQRIHTGEKPYECNECGKGFRCSS QLRQHQSIHTGEKPYQCKECGKGFNNNTKLIQH QRIHTASLAEQLFKASGNHPNWGCCLTISSPGPS VYGPKMNMRGAPNSRLAGGREKRTQDTDFGQC SFLPSHSPSCFEPWNVTDYDSSWYRQKQVLSGV WSSPLSILKLPRTLIRISIHIQEMDTPGEMLMTGR GSLGPTLTTEAPAAAQPGKQGPPGTGRCLQAPGT EPGEQTPEGARELSPLQESSSPGGVKAEEEQRAG AEPGTRPSLARSDDNDHEVGALGLQQGKSPGAG NPEPEQDCAARAPVRAEAVRRMPPGAEAGSVVL DD
3594	A	39	261	RAAMMDTSRVQPIKLAIVIKVLGRTGSQGQCTQ VRVEFMDDTSRSIIRSVKGPVREGDVLTLLESERE ARRLR
3595	A	973	68	GRVGTKHQMADDAGAAGGPGGPGGPGMGNRG GFRGGFGSGIRGRGRGRGRGRGRGARGGKAE

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				DKEWMPVTKLGRLVKDMKIKSLEEIYLFSLPIKE SEIIDFFLGASLKDEVLKIMPVQKQTRAGQRTRF KAFVAIGDYNGHVGLGVKCSKEVATAIRGAIILA KLSIVPVRRGYWGNKIGKPHTVPCKVTGRCGSV LVRLIPAPRGTGIVSAPVPKKLLMMAGIDDCYTS ARGCTATLGNFAKATFDAISKTYSYLTPDLWKE TVFTKSPYQEFTDHLVKTHTRVSVQRTQAPAVA TT
3596	A	106	2960	DERRVGAADMFGRSRSWVGGGHGKTSRNIHSL DHLKYLYHVLTKNTTVTEQNRNLLVETIRSITEIL IWGDQNDSSVFDFFLEKNMFVFFLNILRQKSGRY VCVQLLQTLNILFENISHETSLYYLLSNNYVNSII VHKFDFSDEEIMAYYISFLKTLSLKLNNHTVHFF YNEHTNDFALYTEAIKFFNHPESMVRIAVRTITL NVYKVSLDNQAMLHYIRDKTAVPYFSNLVWFIG SHVIELDDCVQTDEEHRNRGKLSDLVAEHLDHL HYLNDILIINCEFLNDVLTDHLLNRLFLPLYVYSL ENQDKGGERPKISLPVSLYLLSQVFLIIHHAPLVN SLAEVILNGDLSEMYAKTEQDIQRSSAKPSIRCFI KPTETLERSLEMNKHKGKRRVQKRPNYKNVGEE EDEEKGPTEDAQEDAEKAKGTEGGSKGIKTSGES EEIEMVIMERSKLSELAASTSVQEQNTTDEEKSA AATCSESTQWSRPFLDMVYHALDSPDDDYHALF VLCLLYAMSHNKGMDPEKLERIQLPVPNAAEKT TYNHPLAERLIRIMNNAAQPDGKIRLATLELSCL LLKQQVLMSAGCIMKDVHLACLEGAREESVHLV RHFYKGEDIFLDMFEDEYRSMTMKPMNVEYLM MDASILLPPTGTPLTGIDFVKRLPCGDVEKTRRAI RVFFMLRSLSLQLRGEPETQLPLTREEDLIKTDDV LDLNNSDLIACTVITKDGGMVQRSLAVDIYQMS LVEPDVSRLGWGVVKFAGLLQDMQVTGVEDDS RALNITIHKPASSPHSKPFPILQATFIFSDHIRCIIAK QRLAKGRIQARRMKMQRIAALLDLPIQPTTEVLG FGLGSSTSTQHLPFRFYDQGRRGSSDPTVQRSVF ASVDKVPGFAVAQCINEHSSPSLSSQSPPSASGSP SGSGSTSHCDSGGTSSSSTPSTAQSPAGIGHVTQ
3597	A	427	277	GVRRIQHHWAQMHECNVHTYASLFCLFLLHTG KLCCLNSHRHFHCIKYSK
3598	A	1	503	FRPRTKKATAMYLEHYLDSIENLPCELQRNFQL MRELDQRTEDKKAEIDILAAEYISTVKTLSPDQR VERLQKIQNAYSKCKEYSDDKVQLAMQTYEMV DKHIRRLDADLARFEADLKDKMEGSDFESSGGR GLKKGRGQKEKRGSRGRGRRTSEEDTPKKKKH KGG
3599	A	2	3907	KTITALAFSPDGKYLVTGESGHMPAVRVWDVAE HSQVAELQEHKYGVACVAFSPSAKYIVSVGYQH DMIVNVWAWKKNIVVASNKVSSRVTAVSFSED CSYFVTAGNRHIKFWYLDDSKTSKVNATVPLLG RSGLLGELRNNLFTDVACGRGKKADSTFCITSSG LLCEFSDRRLLDKWVELRVYPEVKDSNQACLPP SSFITCSSDNTIRLWNTESSGVHGSTLHRNILSSDL IKIIYVDGNTQALLDTELPGGDKADASLLDPRVGI RSVCVSPNGQHLASGDRMGTLRVHELQSLSEML KVEAHDSEILCLEYSKPDTGLKLLASASRDRLIH VLDAGREYSLQQTLDEHSSSITAVKFAASDGQVR

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				MISCGADKSIYFRTAQKSGDGVQFTRTHHVVRK TTLYDMDVEPSWKYTAIGCQDRNIRIFNISSGKQ KKLFKGSQGEDGTLIKVQTDPSGIYIATSCSDKNL SIFDFSSGECVATMFGHSEIVTGMKFSNDCKHLIS VSGDSCIFVWRLSSEMTISMRQRLAELRQRQRGG KQQGPSSPQRASGPNRHQAPSMLSPGPALSSDSD KEGEDEGTEEELPALPVLAKSTKKALASVPSPAL PRSLSHWEMSRAQESVGFLDPAPAANPGPRRRG RWVQPGVELSVRSMLDLRQLETLAPSLQDPSQD SLAIIPSGPRKHGQEALETSLTSQNEKPPRPQASQ PCSYPHIIRLLSQEEGVFAQDLEPAPIEDGIVYPEP SDNPTMDTSEFQVQAPARGTLGRVYPGSRSSEK HSPDSACSVDYSSSCLSSPEHPTEDSESTEPLSVD GISSDLEEPAEGDEEEEEEGGMGPYGLQEGSPQ TPDQEQFLKQHFETLASGAAPGAPVQVPERSESR SISSRFLLQVQTRPLREPSPSSSSLALMSRPAQVPQ ASGEQPRGNGANPPGAPPEVEPSSGNPSPQQAAS VLLPRCRLNPDSSWAPKRVATASPFSGLQKAQS VHSLVPQERHEASLQAPSPGALLSREIEAQDGLG SLPPADGRPSRPHSYQNPTTSSMAKISRSISVGEN LGLVAEPQAHAPIRVSPLSKLALPSRAHLVLDIPK PLPDRPTLAAFSPVTKGRAPGEAEKPGFPVGLGK AHSTTERWACLGEGTTPKPRTECQAHPGPSSPCA QQLPVSSLFQGPENLQPPPPEKTPNPMECTKPGA ALSQDSEPAVSLEQCEQLVAELRGSVRQAVRLY HSVAGCKMPSAEQSRIAQLLRDTFSSVRQELEAV AGAVLSSPGSSPGAVGAEQTQALLEQYSELLLRA VERRMERKL
3600	A	1688	916	IPGSTISCSMALCEAAGCGSALLWPRLLLFGDSIT QFSFQQGGWGASLADRLVRKCDVLNRGFSGYN TRWAKIILPRLIRKGNSLDIPVAVTIFFGANDSAL KDENPKQHIPLEEYAANLKSMVQYLKSVDIPENR VILITPTPLCETAWEEQCIIQGCKLNRLNSVVGEY ANACLQVAQDCGTDVLDLWTLMQDSQDFSSYL SDGLHLSPKGNEFLFSHLWPLIEKKVSSLPLLLPY WRDVAEAKPELSLLGDGDH
3601	A	44	223	VHFPLIPQLAKCFWTMNRAARNKSEKRYYSEFL QIAHLFNYGLSSFLREFIIFLIKLLQ
3602	A	37	1124	VPKPASGKRRLEFRPQDSKACAATPHSPGRITSR TRGSQKVRSVPPRLPWAQASASTDWEGLRGVPG PALRRENFLEAAASGRSGRTPTGGVGFRDVGGP HFPIFPAAHFLWCNLHTPRRPACNAPWHSPVGEI SPPPRESQLRRDPEVHFESPAHPLGFRLLPGRGLP ANAVTVETAAMAAPRQIPSHIVRLKPSCSTDSSF TRTPVPTVSLASRELPVSSWQVTEPSSKNLWEQI CKEYEAEQPPFPEGYKVKQEPVITVAPVEEMLFH GFSAEHYFPVSHFTMISRTPCPQDKSETINPKTCS PKEYLETFIFPVLLPGMASLLHQAKKEKCFEVVL QMTPSGGKACVWGHLPSSSHTI
3603	A	286	587	NISNKAEVSSHPSVISHSMDSFGQPRPEDNQSVLR RMQKKYWKTKQVFIKATGKKEDEHLVASDAEL DAKLEVFHSVQETCTELLKIIEKYQLRLNGMKS
3604	A	103	2440	QPRRRVFPAAGRGPGRKCSQWGRQASVSFEDVT VDFSKEEWQHLDPAQRRLYWDVTLENYSHLLS VGYYQIPKSEAAFKLEQGEGPWMLEGEAPHQSCS

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				GEAIGKMQQQGIPGGIFFHCERFDQPIGEDSLCSI LEELWQDNDQLEQRQENQNNLLSHVKVLIKERG YEHKNIEKIIHVTTKLVPSIKRLHNCDTILKHTLN SHNHNRNSATKNLGKIFGNGNNFPHSPSSTKNEN AKTGANSCEHDHYEKHLSHKQAPTHHQKIHPEE KLYVCTECVMGFTQKSHLFEHQRIHAGEKSREC DKSNKVFPQKPQVDVHPSVYTGEKPYLCTQCGK VFTLKSNLITHQKIHTGQKPYKCSECGKAFFQRS DLFRHLRIHTGEKPYECSECGKGFSQNSDLSIHQ KTHTGEKHYECNECGKAFTRKSALRMHQRIHTG EKPYVCADCGKAFIQKSHFNTHQRIHTGEKPYEC SDCGKSFTKKSQLHVHQRIHTGEKPYICTECGKV FTHRTNLTTHQKTHTGEKPYMCAECGKAFTDQS NLIKHQKTHTGEKPYKCNGCGKAFIWKSRLKIH QKSHIGERHYECKDCGKAFIQKSTLSVHQRIHTG EKPYVCPECGKAFIQKSHFIAHHRIHTGEKPYECS DCGKCFTKKSQLRVHQKIHTGEKPNICAECGKAF TDRSNLITHQKIHTREKPYECGDCGKTFTWKSRL NIHQKSHTGERHYECSKCGKAFIQKATLSMHQII HTGKKPYACTECQKAFTDRSNLIKHQKMHSGEK RYKASD
3605	A	3	322	SFRMSGRGKGGKGLGKGGAKRHRKVLRDNIQGI TKPAIRRLARRGGVKRISGLIYEETRGVLKVFLEN VIRDAVTYTEHAKRKTVTAMDVVYALKRQGRT LYGFGG
3606	A	1	1749	VPVTAEAKLMGFTQGCVTFEDVAIYFSQEEWGL LDEAQRLLYRDVMLENFALITALVCWHGMEDE ETPEQSVSVEGVPQVRTPEASPSTQKIQSCDMCV PFLTDILHLTDLPGQELYLTGACAVFHQDQKHHS AEKPLESDMDKASFVQCCLFHESGMPFTSSEVG KDFLAPLGILQPQAIANYEKPNKISKCEEAFHVGI SHYKWSQCRRESSHKHTFFHPRVCTGKRLYESS KCGKACCCECSLVQLQRVHPGERPYECSECGKS FSQTSHLNDHRRIHTGERPYVCGQCGKSFSQRAT LIKHHRVHTGERPYECGECGKSFSQSSNLIEHCRI HTGERPYECDECGKAFGSKSTLVRHQRTHTGEK PYECGECGKLFRQSFSLVVHQRIHTTARPYECGQ CGKSFSLKCGLIQHQLIHSGARPFECDECGKSFSQ RTTLNKHHKVHTAERPYVCGECGKAFMFKSKL VRHQRTHTGERPFECSECGKFFRQSYTLVEHQKI HTGLRPYDCGQCGKSFIQKSSLIQHQVVHTGERP YECGKCGKSFTQHSGLILHRKSHTVERPRDSSKC GKPYSPRSNIV
3607	A	92	331	AMAGPGPGPGDPDEQYDFLFKLVLVGDASVGKT CVVQRFKTGAFSERQGSTIGVDFTMKTLEIQGKR VKLQIWDTAGQER
3608	A	545	379	AIKGYIHLSAPRNRYMHTTASNGRMLFMKVTM YMRRGVQIMGWSVRMAFMACFTQ
3609	A	118	873	VWMAWQVSLLELEDRLQCPICLEVFKESLMLQC GHSYCKGCLVSLSYHLDTKVRCPMCWQVVDGS SSLPNVSLAWVIEALRLPGDPEPKVCVHHRNPLS LFCEKDQELICGLCGLLGSHQHHPVTPVSTVCSR MKEELAALFSELKQEQKKVDELIAKLVKNRTRIV NESDVFSWVIRREFQELRHPVDEEKARCLEGIGG HTRGLVASLDMQLEQAQGTRERLAQAECVLEQF

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				GNEDHHEFIWKFHSMASR
3610	A	2	987	DPRVRPPLLQPPPPLLPRLVILKMAPLDLDKYVEI ARLCKYLPENDLKRLCDYVCDLLLEESNVQPVS TPVTVCGDIHGQFYDLCELFRTGGQVPDTNYIFM GDFVDRGYYSLETFTYLLALKAKWPDRITLLRG NHESRQITQVYGFYDECQTKYGNANAWRYCTK VFDMLTVAALIDEQILCVHGGLSPDIKTLDQIRTI ERNQEIPHKGAFCDLVWSDPEDVDTWAISPRGA GWLFGAKVTNEFVHINNLKLICRAHQLVHEGYK FMFDEKLVTVWSAPNYCYRCGNIASIMVFKDVN TREPKLFRAVPDSERVIPPRTTTPYFL
3611	A	2459	869	AEKMTAELREAMALAPWGPVKVKKEEEEEENF PGQASSQQVHSENIKVWAPVQGLQTGLDGSEEE EKGQNISWDMAVVLKATQEAPAASTLGSYSLPG TLAKSEILETHGTMNFLGAETKNLQLLVPKTEIC EEAEKPLIISERIQKADPQGPELGEACEKGNMLK RQRIKREKKDFRQVIVNDCHLPESFKEEENQKCK KSGGKYSLNSGAVKNPKTQLGQKPFTCSVCGKG FSQSANLVVHQRIHTGEKPFECHECGKAFIQSAN LVVHQRIHTGQKPYVCSKCGKAFTQSSNLTVHQ KIHSLEKTFKCNECEKAFSYSSQLARHQKVHITE KCYECNECGKTFTRSSNLIVHQRIHTGEKPFACN DCGKAFTQSANLIVHQRSHTGEKPYECKECGKA FSCFSHLIVHQRIHTAEKPYDCSECGKAFSQLSCL IVHQRIHSGDLPYVCNECGKAFTCSSYLLIHQRIH NGEKPYTCNECGKAFRQRSSLTVHQRTHTGEKP YECEKCGAAFISNSHLMRHHRTHLVE
3612	A	318	2245	SPMAEAALVNTPQIPMVTEEFVKPSQGHVTFEDI AVYFSQEEWGLLDEAQRCLYHDVMLENFSLMA SVGCLHGIEAEEAPSEQTLSAQGVSQARTPKLGP SIPNAHSCEMCILVMKDILYLSEHQGTLPWQKPY TSVASGKWFSFGSNLQQHQNQDSGEKHIRKEESS ALLLNSCKIPLSDNLFPCKDVEKDFPTILGLLQHQ TTHSRQEYAHRSRETFQQRRYKCEQVFNEKVHV TEHQRVHTGEKAYKRREYGKSLNSKYLFVEHQR THNAEKPYVCNICGKSFLHKQTLVGHQQRIHTRE RSYVCIECGKSLSSKYSLVEHQRTHNGEKPYVCN VCGKSFRHKQTFVGHQQRIHTGERPYVCMECGK SFIHSYDRIRHQRVHTGEGAYQCSECGKSFIYKQ SLLDHHRIHTGERPYECKECGKAFIHKKRLLEHQ RIHTGEKPYVCIICGKSFIRSSDYMRHQRIHTGER AYECSDCGKAFISKQTLLKHHKIHTRERPYECSE CGKGFYLEVKLLQHQRIHTREQLCECNECGKVF SHQKRLLEHQKVHTGEKPCECSECGKCFRHRTS LIQHQKVHSGERPYNCTACEKAFIYKNKLVEHQ RIHTGEKPYECGKCGKAFNKRYSLVRHQKVHIT EEP
3613	A	817	3345	NQSHPDSETVTVEGGRRKMKSNQERSNECLPPK KREIPATSRSSEEKAPTLPSDNHRVEGTAWLPGN PGGRGHGGGRHGPAGTSVELGLQQGIGLHKALS TGLDYSPPSAPRSVPVATTLPAAYATPQPGTPVSP VQYAHLPHTFQFIGSSQYSGTYASFIPSQLIPPTAN PVTSAVASAAGATTPSQRSQLEAYSTLLANMGS LSQTPGHKAEQQQQQQQQQQQQQQQQQQQQQQ QQQHQQQQQQQQQQQQQQQHLSRAPGLITPGSPP

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				PAQQNQYVHISSSPQNTGRTASPPAIPVHLHPHQ TMIPHTLTLGPPSQVVMQYADSGSHFVPREATK KAESSRLQQAIQAKEVLNGEMEKSRRYGAPSSA DLGLGKAGGKSVPHPYESRHVVVHPSPSDYSSR DPSGVRASVMVLPNSNTPAADLEVQQATHREAS PSTLNDKSGLHLGKPGHRSYALSPHTVIQTTHSA SEPLPVGLPATAFYAGTQPPVIGYLSGQQQAITY AGSLPQHLVIPGTQPLLIPVGSTDMEASGAAPAIV TSSPQFAAVPHTFVTTALPKSENFNPEALVTQAA YPAMVQAQIHLPVVQSVASPAAAPPTLPPYFMK GSIIQLANGELKKVEDLKTEDFIQSAEISNDLKIDS STVERIEDSHSPGVAVIQFAVGEHRAQVSVEVLV EYPFFVFGQGWSSCCPERTSQLFDLPCSKLSVGD VCISLTLKNLKNGSVKKGQPVDPASVLLKHSKA DGLAGSRHRYAEQENGINQGSAQMLSENGELKF PEKMGLSAAPFLTKIEPSKPAATRKRRWSAPESR KLEKSEDEPPLTLPKPSLIPQEVKICIEGRSNVGK
3614	A	3	114	FFESRLRCKCCEPRGSWARFGCWRLQPEFKPKQ LEG
3615	A	3	1603	DAWALTNQFSDSKQHIEVLKESLTAKEQRAAILQ TEVDALRLRLEEKETMLNKKTKQIQDMAEEKGT QAGEIHDLKDMLDVKERKVNVLQKKIENLQEQL RDKEKQMSSLKERVKSLQADTTNTDTALTTLEE ALAEKERTIERLKEQRDRDEREKQEEIDNYKKDL KDLKEKVSLLQGDLSEKEASLLDLKEHASSLASS GLKKDSRLKTLEIALEQKKEECLKMESQLKKAH EAALEARASPEMSDRIQHLEREITRYKDESSKAQ AEVDRLLEILKEVENEKNDKDKKIAELESLTSRQ VKDQNKKVANLKHKEQVEKKKSAQMLEEARRR EDNLNDSSQQLQDSLRKKDDRIEELEEALRESVQ ITAEREMVLAQEESARTNAEKQVEELLMAMEKV KQELESMKAKLSSTQQSLAEKETHLTNLRAERR KHLEEVLEMKQEALLAAISEKDANIALLELSSSK KKTQEEVAALKREKDRLVQQLKQQTQNRMKLM ADNYEDDHFKSSHSNQTNHKPSPDQDEEEGIWA
3616	A	244	1420	RRRWRARGGLVPTLAWAEATGAYVPGRDKPDL PTWKRNFRSALNRKEGLRLAEDRSKDPHDPHKI YEFVNSGVGDFSQPDTSPDTNGGGSTSDTQEDIL DELLGNMVLAPLPDPGPPSLAVAPEPCPQPLRSPS LDNPTPFPNLGPSENPLKRLLVPGEEWEFEVTAF YRGRQVFQQTISCPEGLRLVGSEVGDRTLPGWP VTLPDPGMSLTDRGVMSYVRHVLSCLGGGLAL WRAGQWLWAQRLGHCHTYWAVSEELLPNSGH GPDGEVPKDKEGGVFDLGPFIVGSLGPPDLITFTE GSGRSPRYALWFCVGESWPQDQPWTKRLVMVK VVPTCLRALVEMARVGGASSLENTVDLHISNSHP LSLTSDQYKAYLQDLVEGMDFQGPGES
3617	A	852	304	RGGLLSKMARVLKAAAANAVGLFSRLQAPIPTV RASSTSQPLDQVTGSVWNLGRLNHVAIAVPDLE KAAAFYKNILGAQVSEAVPLPEHGVSVVFVNLG NTKMELLHPLGRDSPIAGFLQKNKAGGMHHICIE VDNINAAVMDLKKKKIRSLSEEVKIGAHGKPVIF LHPKDCGGVLVELEQA
3618	A	3	5992	DNIDETYGVNVQFESDEEEGDEDVYGEVREEAS DDDMEGDEAVVRCTLSANMYVDEILVWCASEL

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				NIPEFFPLESPHKKVGYGLSSRTWLQGGGKVIEA GRDLLVASGELMSSKKKDLHPRDIDAFWLQRQL SRFYDDAIVSQKKADEVLEILKTASDDRECENQL VLLLGFNTFDFIKVLRQHRMMILYCTLLASAQSE AEKERIMGKMEADPELSKFLYQLHETEKEDLIRE ERSRRERVRQSRMDTDLETMDLDQGGEALAPRQ VLDLEDLVFTQGSHFMANKRCQLPDGSFRRQRK GYEEVHVPALKPKPFGSEEQLLPVEKLPKYAQA GFEGFKTLNRIQSKLYRAALETDENLLLCAPTGA GKTNVALMCMLREIGKHINMDGTINVDDFKIIYI APMRSLVQEMVGSFGKRLATYGITVAELTGDHQ LCKEEISATQIIVCTPEKWDIITRKGGERTYTQLV RLIILDEIHLLHDDRGPVLEALVARAIRNIEMTQE DVRLIGLSATLPNYEDVATFLRVDPAKGLFYFDN SFRPVPLEQTYVGITEKKAIKRFQIMNEIVYEKIM EHAGKNQVLVFVHSRKETGKTARAIRDMCLEKD TLGLFLREGSASTEVLRTEAEQCKNLELKDLLPY GFAIHHAGMTRVDRTLVEDLFGDKHIQVLVSTA TLAWGVNLPAHTVIIKGTQVYSPEKGRWTELGA LDILQMLGRAGRPQYDTKGEGILITSHGELQYYL SLLNQQLPIESQMVSKLPDMLNAEIVLGNVQNA KDAVNWLGYAYLYIRMLRSPTLYGISHDDLKGD PLLDQRRLDLVHTAALMLDKNNLVKYDKKTGN FQVTELGRIASHYYITNDTVQTYNQLLKPTLSEIE LFRVFSLSSEFKNITVREEEKLELQKLLERVPIPVK ESIEEPSAKINVLLQAFISQLKLEGFALMADMVY VTQSAGRLMRAIFEIVLNRGWAQLTDKTLNLCK MIDKRMWQSMCPLRQFRKLPEEVVKKIEKKNFP FERLYDLNHNEIGELIRMPKMGKTIHKYVHLFPK LELSVHLQPITRSTLKVELTITPDFQWDEKVHGSS EAFWILVEDVDSEVILHHEYFLLKAKYAQDEHLI TFFVPVFEPLPPQYFIRVVSDRWLSCETQLPVSFR HLILPEKYPPPTELLDLQPLPVSALRNSAFESLYQ DKFPFFNPIQTQVFNTVYNSDDNVFVGAPTGSGK TICAEFAILRMLLQNSEGRCVYITPMRLWQEQVY MDWYEKFQDRLNKKVVLLTGETSTDLKLLGKG NIIISTPEKWDILSRRWKQRKNVQNINLFVVDEV HLIGGENGPVLEVICSRMRYISSQIERPIRIVALSSS LSNAKDVAHWLGCSATSTFNFHPNVRPVPLELHI QGFNISHTQTRLLSMAKPVFHAITKHSPKKPVIVF VPSRKQTRLTAIDILTTCAADIQRQRFLHCTEKDL IPYLEKLSDSTLKETLLNGVGYLHEGLSPMERRL VEQLFSSGAIQVVVASRSLCWGMNVAAHLVIIM DTLYYNGKIHAYVDYPIYDVLQMVGHANRPLQ DDEGRCVIMCQGSKKDFFKKFLYEPLPVESHLD HCMHDHFNAEIVTKTIENKQDAVDYLTWTFLYR RMTQNPNYYNLQGISHRHLSDHLSELVEQTLSDL EQSKCISIEDEMDVAPLNLGMIAAYYYINYTTIEL FSMSLNAKTKVRGLIEIISNAAEYENIPIRHHEDN LLRQLAQKVPHKLNNPKFNDPHVKTNLLLQAHL SRMQLSAELQSDTEEILSKAIRLIQACVDVLSSNG WLSPALAAMELAQMVTQAMWSEDSYLRRLPPF PSGLFKRCTDKGVESVFDIMEMEDEERNALLQLT DSQIADVARFCNRYPNIELSYEVVDKDSIRSGGP VVVLVQLEREEEVTGPVIAPLFPQKREEGWWVV

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				IGDAKSNSLISIKRLTLQQKAKVKLDFVAPATGG RHNTLYFMSDAYMGCDQEYKFSVDVKEAETDS DSD
3619	A	3	5992	DNIDETYGVNVQFESDEEEGDEDVYGEVREEAS DDDMEGDEAVVRCTLSANMYVDEILVWCASEL NIPEFFPLESPHKKVGYGLSSRTWLQGGGKVIEA GRDLLVASGELMSSKKKDLHPRDIDAFWLQRQL SRFYDDAIVSQKKADEVLEILKTASDDRECENQL VLLLGFNTFDFIKVLRQHRMMILYCTLLASAQSE AEKERIMGKMEADPELSKFLYQLHETEKEDLIRE ERSRRERVRQSRMDTDLETMDLDQGGEALAPRQ VLDLEDLVFTQGSHFMANKRCQLPDGSFRRQRK GYEEVHVPALKPKPFGSEEQLLPVEKLPKYAQA GFEGFKTLNRIQSKLYRAALETDENLLLCAPTGA GKTNVALMCMLREIGKHINMDGTINVDDFKIIYI APMRSLVQEMVGSFGKRLATYGITVAELTGDHQ LCKEEISATQIIVCTPEKWDIITRKGGERTYTQLV RLIILDEIHLLHDDRGPVLEALVARAIRNIEMTQE DVRLIGLSATLPNYEDVATFLRVDPAKGLFYFDN SFRPVPLEQTYVGITEKKAIKRFQIMNEIVYEKIM EHAGKNQVLVFVHSRKETGKTARAIRDMCLEKD TLGLFLREGSASTEVLRTEAEQCKNLELKDLLPY GFAIHHAGMTRVDRTLVEDLFGDKHIQVLVSTA TLAWGVNLPAHTVIIKGTQVYSPEKGRWTELGA LDILQMLGRAGRPQYDTKGEGILITSHGELQYYL SLLNQQLPIESQMVSKLPDMLNAEIVLGNVQNA KDAVNWLGYAYLYIRMLRSPTLYGISHDDLKGD PLLDQRRLDLVHTAALMLDKNNLVKYDKKTGN FQVTELGRIASHYYITNDTVQTYNQLLKPTLSEIE LFRVFSLSSEFKNITVREEEKLELQKLLERVPIPVK ESIEEPSAKINVLLQAFISQLKLEGFALMADMVY VTQSAGRLMRAIFEIVLNRGWAQLTDKTLNLCK MIDKRMWQSMCPLRQFRKLPEEVVKKIEKKNFP FERLYDLNHNEIGELIRMPKMGKTIHKYVHLFPK LELSVHLQPITRSTLKVELTITPDFQWDEKVHGSS EAFWILVEDVDSEVILHHEYFLLKAKYAQDEHLI TFFVPVFEPLPPQYFIRVVSDRWLSCETQLPVSFR HLILPEKYPPPTELLDLQPLPVSALRNSAFESLYQ DKFPFFNPIQTQVFNTVYNSDDNVFVGAPTGSGK TICAEFAILRMLLQNSEGRCVYITPMRLWQEQVY MDWYEKFQDRLNKKVVLLTGETSTDLKLLGKG NIIISTPEKWDILSRRWKQRKNVQNINLFVVDEV HLIGGENGPVLEVICSRMRYISSQIERPIRIVALSSS LSNAKDVAHWLGCSATSTFNFHPNVRPVPLELHI QGFNISHTQTRLLSMAKPVFHAITKHSPKKPVIVF VPSRKQTRLTAIDILTTCAADIQRQRFLHCTEKDL IPYLEKLSDSTLKETLLNGVGYLHEGLSPMERRL VEQLFSSGAIQVVVASRSLCWGMNVAAHLVIIM DTLYYNGKIHAYVDYPIYDVLQMVGHANRPLQ DDEGRCVIMCQGSKKDFFKKFLYEPLPVESHLD HCMHDHFNAEIVTKTIENKQDAVDYLTWTFLYR RMTQNPNYYNLQGISHRHLSDHLSELVEQTLSDL EQSKCISIEDEMDVAPLNLGMIAAYYYINYTTIEL FSMSLNAKTKVRGLIEIISNAAEYENIPIRHHEDN LLRQLAQKVPHKLNNPKFNDPHVKTNLLLQAHL

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				SRMQLSAELQSDTEEILSKAIRLIQACVDVLSSNG WLSPALAAMELAQMVTQAMWSEDSYLRRLPPF PSGLFKRCTDKGVESVFDIMEMEDEERNALLQLT DSQIADVARFCNRYPNIELSYEVVDKDSIRSGGP VVVLVQLEREEEVTGPVIAPLFPQKREEGWWVV IGDAKSNSLISIKRLTLQQKAKVKLDFVAPATGG RHNTLYFMSDAYMGCDQEYKFSVDVKEAETDS DSD
3620	A	1205	323	VIKMALAARLLPQFLHSRSLPCGAVRLRTPAVAE VRLPSATLCYFCRCRLGLGAALFPRSARALAASA LPAQGSRWPVLSSPGLPAAFASFPACPQRSYSTE EKPQQHQKTKMIVLGFSNPINWVRTRIKAFLIWA YFDKEFSITEFSEGAKQAFAHVSKLLSQCKFDLL EELVAKEVLHALKEKVTSLPDNHKNALAANIDEI VFTSTGDISIYYDEKGRKFVNILMCFWYLTSANIP SETLRGASVFQVKLGNQNVETKQLLSASYEFQR EFTQGVKPDWTIARIEHSKLLE
3621	A	2	2995	SSSRSRHSSISPVRLPLNSSLGAELSRKKKERAAA AAAAKMDGKESSYERSGSYSGRSPSPYGRRRSSS PFLSKRSLSRSPLPSRKSMKSRSRSPAYSRHSSSH SKKKRSSSRSRHSSISPVRLPLNSSLGAELSRKKK ERAAAAAAAKMDGKESSYERSGSYSGRSPSPYG RRRSSSPFLSKRSLSRSPLPSRKSMKSRSRSPAYS RHSSSHSKKKRSSSRSRHSSISPVRLPLNSSLGAEL SRKKKERAAAAAAAKMDGKESKGSPVFLPRKE NSSVEAKDSGLESKKLPRSVKLEKSAPDTELVNV THLNTEVKNSSDTGKVKLDENSEKHLVKDLKAQ GTRDSKPIALKEEIVTPKETETSEKETPPPLPTIASP PPPLPTTTPPPQTPPLPPLPPIPALPQQPPLPPSQPA FSQVPASSTSTLPPSTHSKTSAVSSQANSQPPVQV SVKTQVSVTAAIPHLKTSTLPPLPLPPLLPGDDDM DSPKETLPSKPVKKEKEQRTRHLLTDLPLPPELPG GDLSPPDSPEPKAITPPQQPYKKRPKICCPRYGER RQTESDWGKRCVDKFDIIGIIGEGTYGQVYKAKD KDTGELVALKKVRLDNEKEGFPITAIREIKILRQL IHRSVVNMKEIVTDKQDALDFKKDKGAFYLVFE YMDHDLMGLLESGLVHFSEDHIKSFMKQLMEGL EYCHKKNFLHRDIKCSNILLNNSGQIKLADFGLA RLYNSEESRPYTNKVITLWYRPPKLLLGEERYTP AIDVWSCGCILGELFTKKPIFQANLELAQLELISR LCGSPCPAVWPDVIKLPYFNTMKPKKQYRRRLR EEFSFIPSAALDLLDHMLTLDPSKRCTAEQTLQSD FLKDVELSKMAPPDLPHWQDCHELWSKKRRRQ RQSGVVVEEPPPSKTSRKETTSGTSTEPVKNSSPA PPQPAPGKVESGAGDAIGLADITQQLNQSELAVL LNLLQSQTDLSIPQMAQLLNIHSNPEMQQQLEAL NQSISALTEATSQQQDSETMAPEESLKEAPSAPVI LPSAEQTTLEASSTPADMQNILAVLLSQLMKTQE PAGSLEENNSDKNSGPQGPRRTPTMPQEEAAGRS NGGNAL
3622	A	16	390	TPERGSAYPETAAVRRPAGECPITMSDLEAKLST EHLGDKIKDEDIKLRVIGQDSSEIHFKVKMTTPLK KLKKSYCQRQGVPVNSLRFLFEGQRIADNHTPEE LGMEEEDVIEVYQEQIGGHSTV
3623	A	2	1544	PPPAPGPDGLNEGCLHRLSMPHQRPRTCAMNPE

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				LTMESLGTLHGARGGGSGGGGGGGGGGGGGGGP GHEQELLASPSPHHARRGPRGSLRGPPPPPTAHQ ELGTAAAAAAAASRSAMVTSMASILDGGDYRPE LSIPLHHAMSMSCDSSPPGMGMSNTYTTLTPLQP LPPISTVSDKFHHPHPHHHPHHHHHHHHQRLSGN VSGSFTLMRDERGLPAMNNLYSPYKEMPGMSQS LSPLAATPLGNGLGGLHNAQQSLPNYGPPGHDK MLSPNFDAHHTAMLTRGEQHLSRGLGTPPAAM MSHLNGLHHPGHTQSHGPVLAPSRERPPSSSSGS QVATSGQLEEINTKEVAQRITAELKRYSIPQAIFA QRVLCRSQGTLSDLLRNPKPWSKLKSGRETFRR MWKWLQEPEFQRMSALRLAACKRKEQEPNKDR NNSQKKSRLVFTDLQRRTLFAIFKENKRPSKEMQ ITISQQLGLELTTVSNFFMNARRRSLEKWQDDLS TGGSSSTSSTCTKA
3624	A	27	2152	SARKAEAATSGTAARDGSVGRNLVPPPSASAPK AEVESNEKDNRPEEEEQVIHEDDERPSEKNEFSR RKRSKSEDMDNVQSKRRRYMEEEYEAEFQVKIT AKGDINQKLQKVIQWLLEEKLCALQCAVFDKTL AELKTRVEKIECNKRHKTVLTELQAKIARLTKRF EAAKEDLKKRHEHPPNPPVSPGKTVNDVNSNNN MSYRNAGTVRQMLESKRNVSESAPPSFQTPVNT VSSTNLVTPPAVVSSQPKLQTPVTSGSLTATSVLP APNTATVVATTQVPSGNPQPTISLQPLPVILHVPV AVSSQPQLLQSHPGTLVTNQPSGNVEFISVQSPPT VSGLTKNPVSLPSLPNPTKPNNVPSVPSPSIQRNP TASAAPLGTTLAVQAVPTAHSIVQATRTSLPTVG PSGLYSPSTNRGPIQMKIPISAFSTSSAAEQNSNTT PRIENQTNKTIDASVSKKAADSTSQCGKATGSDS SGVIDLTMDDEESGASQDPKKLNHTPVSTMSSSQ PVSRPLQPIQPAPPLQPSGVPTSGPSQTTIHLLPTA PTTVNVTHRPVTQVTTRLPVPRAPANHQVVYTT LPAPPAQAPLRGTVMQAPAVRQVNPQNSVTVRV PQTTTYVVNNGLTLGSTGPQLTVHHRPPQVHTEP PRPVHPAPLPEAPQPQRLPPEAGSTSRPSEATLEV SHAFRVKMAIVLVMECPGGGSKLCHC
3625	A	210	1115	ASPFLRPQGHDSGEREPFSQTPGLMQPFSIPVQIT LQGSRRRQGRTAFPASGKKRETDYSDGDPLDVH KRLPSSTGEDRAVMLGFAMMGFSVLMFFLLGTT ILKPFMLSIQREESTCTAIHTDIMDDWLDCAFTCG VHCHGQGKYPCLQVFVNLSHPGQKALLHYNEE AVQINPKCFYTPKCHQDRNDLLNSALDIKEFFDH KNGTPFSCFYSPASQSEDVILIKKYDQMAIFHCLF WPSLTLLGGALIVGMVRLTQHLSLLCEKYSTVV RDEVGGKVPYIEQHQFKLCIMRRSKGRAEKS
3626	A	9	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEG FLSAEECVAMQQRIGEIVAEMDVPLHCRTEFSTQ EEEQLRAQGSTDYFLSSGDKIRFFFEKGVFDEKG NFLVPPEKSINKIGHALHAHDPVFKSITHSFKVQT LARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQD ASFLYTEPLGRVLGVWIAVEDATLENGCLWFIPG SHTSGVSRRMVRAPVGSAPGTSFLGSEPARDNSL FVPTPVQRGALVLIHGEVVHKSKQNLSDRSRQA YTFHLMEASGTTWSPENWLQPTAELPFPQLYT
3627	A	231	644	INSSPRTGRDHQELNLHTERDSRSQRAVLKIPRQ

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				NPGIFYWIFLPSRSHSASHGSRQRQVSCQGTQDEI LKMRNTFAELKNSLEALSSRMDQAEERIGTQAG VQWRDHGSLQPQPPEFKQCFHLSLPSSWDYRAC LS
3628	A	2	810	GCKHLLQNSWYDPRVREADRVGQRARRPRAAM DWLMGKSKAKPNGKKPAAEERKAYLEPEHTKA RITDFQFKELVVLPREIDLNEWLASNTTTFFHHIN LQYSTISEFCTGETCQTMAVCNTQYYWYDERGK KVKCTAPQYVDFVMSSVQKLVTDEDVFPTKYG REFPSSFESLVRKICRHLFHVLAHIYWAHFKETLA LELHGHLNTLYVHFILFAREFNLLDPKETAIMDD LTEVLCSGGRRGSTVGAVGMGPAAGAPGAQNH VKER
3629	A	699	1604	CSHGSSAVSAWSPLFQASEVERQLSMQVHALRE DFREKNSSTNQHIIRLESLQAEIKMLSDRKRELEH RLSATLEENDLLQGTVEELQDRVLILERQGHDKD LQLHQSQLELQEVRLSCRQLQVKVEELTEERSLQ SSAATSTSLLSEIEQSMEAEELEQEREQLTLLSVE MTALKEERDRLRVTSEDKEPKEQLQKAIRDRDE AIAKKNAVELELAKCRMDMMSLNSQLLDAIQQ KLNLSQQLEAWQDDMHRVIDRQLMDTHLKERS QPAAALCRGHSAGRGDEPSIAEGKRLFSFFRKI
3630	A	423	1	PAKVLTLDIYLSKTEGAQVDEPVVITPRAEDCGD WDDMEKRSSGRRSGRRRGSQKSTDSPGADAELP ESAARDDAVFDDEVAPNAASDNASAEKKVKSPR AALDGGVASAASPESKPSPGTKGQLRGESDRSK QPPPASSP
3631	A	2082	674	WSGFWQLPGVRGVGSAPGGDGAEFTSRRGSSRR PGAACPGCRGAGSERAPGGMGRRRAPELYRAPF PLYALQVDPSTGLLIAAGGGGAAKTGIKNGVHF LQLELINGRLSASLLHSHDTETRATMNLALAGDI LAAGQDAHCQLLRFQAHQQQGNKAEKAGSKEQ GPRQRKGAAPAEKKCGAETQHEGLELRVENLQA VQTDFSSDPLQKVVCFNHDNTLLATGGTDGYVR VWKVPSLEKVLEFKAHEGEIEDLALGPDGKLVT VGRDLKASVWQKDQLVTQLHWQENGPTFSSTP YRYQACRFGQVPDQPAGLRLFTVQIPHKRLRQPP PCYLTAWDGSNFLPLRTKSCGHEVVSCLDVSES GTFLGLGTVTGSVAIYIAFSLQCLYYVREAHGIV VTDVAFLPEKGRGPELLGSHETALFSVAVDSRCQ LHLLPSRRSVPVWLLLLLCVGLIIVTILLLQSAFPG FL
3632	A	942	40	PWCQRVEVRSCGSSKRSCSRWSGSSWDGSRSLG RGLNHTSLNRSPPFTPDTMTHCCSPCCQPTCCRT TCCRTTCWKPTTVTTCSSTPCCQPSCCVPSCCQP CCHPTCCQNTCCRTTCCQPTCVASCCQPSCCSTP CCQPTCCGSSCCGQTSCGSSCCQPICGSSCCQPCC HPTCYQTICFRTTCCQPTCCQPTCCRNTSCQPTCC GSSCCQPCCHPTCCQTICRSTCCQPSCVTRCCSTP CCQPTCGGSSCCSQTCNESSYCLPCCRPTCCQTT CYRTTCCRPSCCCSPCCVSSCCQPSCC
3633	A	605	3004	GPEGYRGRRARHPSLGSTTGHCGGGRGAEGTGT DPAAPAARLNVDGLLVYFPYDYIYPEQFSYMRE LKRTLDAKGHGVLEMPSGTGKTVSLLALIMAYQ RAYPLEVTKLIYCSRTVPEIEKVIEELRKLLNFYE

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				KQEGEKLPFLGLALSSRKNLCIHPEVTPLRFGKD VDGKCHSLTASYVRAQYQHDTSLPHCRFYEEFD AHGREVPLPAGIYNLDDLKALGRRQGWCPYFLA RYSILHANVVVYSYHYLLDPKIADLVSKELARK AVVVFDEAHNIDNVCIDSMSVNLTRRTLDRCQG NLETLQKTVLRIKETDEQRLRDEYRRLVEGLREA SAARETDAHLANPVLPDEVLQEAVPGSIRTAEHF LGFLRRLLEYVKWRLRVQHVVQESPPAFLSGLA QRVCIQRKPLRFCAERLRSLLHTLEITDLADFSPL TLLANFATLVSTYAKGFTIIIEPFDDRTPTIANPIL HFSCMDASLAIKPVFERFQSVIITSGTLSPLDIYPK ILDFHPVTMATFTMTLARVCLCPMIIGRGNDQVA ISSKFETREDIAVIRNYGNLLLEMSAVVPDGIVAF FTSYQYMESTVASWYEQGILENIQRNKLLFIETQ DGAETSVALEKYQEACENGRGAILLSVARGKVS EGIDFVHHYGRAVIMFGVPYVYTQSRILKARLEY LRDQFQIRENDFLTFDAMRHAAQCVGRAIRGKT DYGLMVFADKRFARGDKRGKLPRWIQEHLTDA NLNLTVDEGVQVAKYFLRQMAQPFHREDQLGL SLLSLEQLESEETLKRIEQIAQQL
3634	A	159	384	LKMSSKTASTNNIAQARRTVQQLRLEASIERIKV SKASADLMSYCEEHARSDPLLIGIPTSENPFKDKK TCIIL
3635	A	5	409	TELSQLEKAHPPADMGRRKSKRKPPPKKKMTGT LETQFTCPFCNHEKSCDVKMDRARNTGVISCTV CLEEFQTPITCILGNLGFFQRVGRGLESGPCSSGP LCALVQGQSRPEEQVPPSDFCGVRRCRAGFQCQ
3636	A	48	282	DHLKSCYQDSHEDPTKMKRFLFLLLTISLLVMVQ IQTGLSGQNDTSQTSSPSASSSMSGGIFLFFVANAI IHLFCFS
3637	A	1	1248	ARAGSVVGSAAARGPPAGCRCERAARLPSSPAR RRRCDWVEDGAGRMEILMTVSKFASICTMGAN ASALEKEIGPEQFPVNEHYFGLVNFGNTCYCNSV LQALYFCRPFREKGLAYKSQPRKKESLLTCLADL FHSIATQKKKVGVIPPKKFITRLRKENELFDNYM QQDAHEFLNYLLNTIADILQEERKQEKQNGRLPN GNIDNENNNSTPDPTWVHEIFQGTLTNETRCLTC ETISSKDEDFLDLSVDVEQNTSITHCLRGFSNTET LCSEYKYYCEECRSKQEAHKRMKVKKLPMILAL HLKRFKYMDQLHRYTKLSYRVVFPLELRLFNTS GDATNPDRMYDLVAVVVHCGSGPNRGHYIAIV KSHDFWLLFDDDIVEKIDAQAIEEFYGLTSDISKN SESGYILFYQSRD
3638	A	11	630	PAGIPVSTISSDRRASTDLTRKMKPDETPMFDPNL LKEVDWSQNTATFSPAISPTHPGEGLVLRPLCTA DLNRGFFKVLGQLTETGVVSPEQFMKSFEHMKK SGDYYVTVVEDVTLGQIVATATLIIEHKFIHSCAK RGRVEDVVVSDECRGKQLGNLLLSTLTLLSKKL NCYKITLECLPQNVGFYKKFGYTVSEENYMCRR FLK
3639	A	2	1200	PRVRLLRPSRSRSCRGLLSTRAPGPSPFRSLHSSPL LPHAMKSPFYRCQNTTSVEKGNSAVMGGVLFST GLLGNLLALGLLARSGLGWCSRRPLRPLPSVFY MLVCGLTVTDLLGKCLLSPVVLAAYAQNRSLRV LAPALDNSLCQAFAFFMSFFGLSSTLQLLAMALE

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				CWLSLGHPFFYRRHITLRLGALVAPVVSAFSLAF CALPFMGFGKFVQYCPGTWCFIQMVHEEGSLSV LGYSVLYSSLMALLVLATVLCNLGAMRNLYAM HRRLQRHPRSCTRDCAEPRADGREASPQPLEELD HLLLLALMTVLFTMCSLPVIYRAYYGAFKDVKE KNRTSEEAEDLRALRFLSVISIVDPWIFIIFRSPVFR IFFHKIFIRPLRYRSRCSNSTNMESSL
3640	A	930	182	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEY AIEAIKLGSTAIGIQTSEGVCLAVEKRITSPLMEPS SIEKIVEIDAHIGCAMSGLIADAKTLIDKARVETQ NHWFTYNETMTVESVTQAVSNLALQFGEEDADP GAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFV QCDARAIGSASEGAQSSLQEVYHKSMTLKEAIKS SLIILKQVMEEKLNATNIELATVQPGQNFHMFTK EELEEVIKDI
3641	A	2	1254	PTGQGGRRAEARSCLLSKAMLGRSGYRALPLGD FDRFQQSSFGFLGSQKGCLSPERGGVGTGADVPQ SWPSCLCHGLISFLGFLLLLVTFPISGWFALKIVPT YERMIVFRLGRIRTPQGPGMVLLLPFIDSFQRVDL RTRAFNVPPCKLASKDGAVLSVGADVQFRIWDP VLSVMTVKDLNTATRMTAQNAMTKALLKRPLR EIQMEKLKISDQLLLEINDVTRAWGLEVDRVELA VEAVLQPPQDSPAGPNLDSTLQQLALHFLGGSM NSMAGGAPSPGPADTVEMVSEVEPPAPQVGARS SPKQPLAEGLLTALQPFLSEALVSQVGACYQFNV VLPSGTQSAYFLDLTTGRGRVGHGVPDGIPDVV VEMAEADLRALLCRELRPLGAYMSGRLKVKGD LAMAMKLEAVLRALK
3642	A	1	237	RRGEIDMATEGDVELELETETSGPERPPEKPRKH DSGAADLERVTDYAEEKEIQSSNLETAMSVIGDR RSREQKAKQER
3643	A	94	541	RKERRRRRRMEAVVFVFSLLDCCALIFLSVYFII TLSDLECDYINARSCCSKLNKWVIPELIGHTIVTV LLLMSLHWFIFLLNLPVATWNIYRYIMVPSGNM GVFDPTEIHNRGQLKSHMKEAMIKLGFHLLCFF MYLYSMILALIND
3644	A	95	2808	TSCRHFPITSEDPLNYLLILTVERIYAYQALPLGFL FCSRDPVPEYLNHCGVKYVLISDRASFCALHIFFS PFRNVFRPAAGGGIAPPPRLWFQPSLSDAEMEIPK LLPARGTLQGGGGGGGIPAGGGRVHRGPDSPAGQ VPTRRLLLPRGPQDGGPGRRREEASTASRGPGPS LFAPRPHQPSGGGGGGGGDDFFLVLLDPVGGDVE TAGSGQAAGPVLREEAEEGPGLQGGESGANPAG PTALGPRCLSAVPTPAPISAPGPAAAFAGTVTIHN QDLLLLRFENGVLTLATPPPHAWEPGAAPAQQPG CLIAPQAGFPHAAHPGDCPELPPDLLLAEPAEPAP APAPEEEAEGPAAALGPRGPLGSGPGVVLYLCPE ALCGQTFAKKHQLKMHLLTHSSSQGQRPFKCPL GGCGWTFTTSYKLKRHLQSHDKLRPFGCPAEGC GKSFTTVYNLKAHMKGHEQENSFKCEVCEESFP TQAKLGAHQRSHFEPERPYQCAFSGCKKTFITVS ALFSHNRAHFREQELFSCSFPGCSKQYDKACRLK IHLRSHTGERPFLCDFDGCGWNFTSMSKLLRHKR KHDDDRRFMCPVEGCGKSFTRAEHLKGHSITHL STKPFVCPVAGCCARFSARSSLYIHSKKHLQDVD

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				TWKSRCPISSCNKLFTSKHSMKTHMVKRHKVGQ DLLAQLEAANSLTPSSELTSQRQNDLSDAEIVSLF SDVPDSTSAALLDTALVNSGILTIDVASVSSTLAG HLPANNNNSVGQAVDPPSLMATSDPPQSLDTSLF FGTAATGFQQSSLNMDEVSSVSVGPLGSLDSLA MKNSSPEPQALTPSSKLTVDTDTLTPSSTLCENSV SELLTPAKAEWSVHPNSDFFGQEGETQFGFPNAA GNHGSQKERNLITVTGSSFLV
3645	A	2194	1707	TVSFHKTMASLKCSTVVCVICLEKPKYRCPACRV PYCSVVCFRKHKEQCNPETRPVEKKIRSALPTKT VKPVENKDDDDSIADFLNSDEEEDRVSLQNLKN LGESATLRSLLLNPHLRQLMVNLDQGEDKAKLM RAYMQEPLFVEFADCCLGIVEPSQNEES
3646	A	85	1948	ERGGGKAAAAAAAAAAARALAASGQDPRPHPR APPWDDSGDDDEATTPADKSELHHTLKNLSLKL DDLSTCNDLIAKHGAALQRSLTELDGLKIPSESG EKLKVVNERATLFRITSNAMINACRDFLELAEIHS RKWQRALQYEQEQRVHLEETIEQLAKQHNSLER AFHSAPGRPANPSKSFIEGSLLTPKGEDSEEDEDT EYFDAMEDSTSFITVITEAKEDSRKAEGSTGTSSA DWSSADNVLDGASLVPKGSSKVKRRVRIPNKPN YSLNLWSIMKNCIGRELSRIPMPVNFNEPLSMLQ RLTEDLEYHHLLDKAVHCTSSVEQMCLVAAFSV SSYSTTVHRIAKPFNPMLGETFELDRLDDMGLRS LCEQVSHHPPSAAHYVFSKHGWSLWQEITISSKF RGKYISIMPLGAIHLEFQASGNHYVWRKSTSTVH NIIVGKLWIDQSGDIEIVNHKTNDRCQLKFLPYSY FSKEAARKVTGVVSDSQGKAHYVLSGSWDEQM ECSKVMHSSPSSPSSDGKQKTVYQTLSAKLLWK KYPLPENAENMYYFSELALTLNEHEEGVAPTDS RLRPDQRLMEKGRWDEANTEKQRLEEKQRLSR RRRLEACGPGSSCSSEE
3647	A	46	5007	PTGDACVSTSCELASALSHLDASHLTENLPKAAS ELGQQPMTELDSSSDLISSPGKKGAAHPDPSKTS VDTGQVSRPENPSQPASPRVTKCKARSPVRLPHE GSPSPGEKAAAPPDYSKTRSASETSTPHNTRRVA ALRGAGPGAEGMTPAGAVLPGDPLTSQEQRQGA PGNHSKALEMTGIHAPESSQEPSLLEGADSVSSR APQASLSMLPSTDNTKEACGHVSGHCCPGGSRE SPVTDIDSFIKELDASAARSPSSQTGDSGSQEGSA QGHPPAGAGGGSSCRAEPVPGGQTSSPRRAWAA GAPAYPQWASQPSVLDSINPDKHFTVNKNFLSN YSRNFSSFHEDSTSLSGLGDSTEPSLSSMYGDAE DSSSDPESLTEAPRASARDGWSPPRSRVSLHKED PSESEEEQIEICSTRGCPNPPSSPAHLPTQAAICPAS AKVLSLKYSTPRESVASPREKVACLPGSYTSGPD SSQPSSLLEMSSQEHETHADISTSQNHRPSCAEET TEVTSASSAMENSPLSKVARHFHSPPIILSSPNMV NGLEHDLLDDETLNQYETSINAAASLSSFSVDVP KNGESVLENLHISESQDLDDLLQKPKMIARRPIM AWFKEINKHNQGTHLRSKTEKEQPLMPARSPDS KIQMVSSSQKKGVTVPHSPPQPKTNLENKDLSKK SPAEMLLTNGQKAKCGPKLKRLSLKGKAKVNSE APAANAVKAGGTDHRKPLISPQTSHKTLSKAVS QRLHVADHEDPDRNTTAAPRSPQCVLESKPPLAT

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				SGPLKPSVSDTSIRTFVSPLTSPKPVPEQGMWSRF HMAVLSEPDRGCPTTPKSPKCRAEGRAPRADSG PVSPAASRNGMSVAGNRQSEPRLASHVAADTAQ PRPTGEKGGNIMASDRLERTNQLKIVEISAEAVSE TVCGNKPAESDRRGGCLAQGNCQEKSEIRLYRQ VAESSTSHPSSLPSHASQAEQEMSRSFSMAKLAS SSSSLQTAIRKAEYSQGKSSLMSDSRGVPRNSIPG GPSGEDHLYFTPRPATRTYSMPAQFSSHFGREGH PPHSLGRSRDSQVPVTSSVVPEAKASRGGLPSLA NGQGIYSVKPLLDTSRNLPATDEGDIISVQETSCL VTDKIKVTRRHYCYEQNWPHESTSFFSVKQRIKS FENLANADRPVAKSGASPFLSVSSKPPIGRRSSGS IVSGSLGHPGDAAARLLRRSLSSCSENQSEAGTL LPQMAKSPSIMTLTISRQNPPETSSKGSDSELKKS LGPLGIPTPTMTLASPVKRNKSSVRHTQPSPVSRS KLQELRALSMPDLDKLCSEDYSAGPSAVLFKTEL EITPRRSPGPPAGGVSCPEKGGNRACPGGSGPKT SAAETPSSASDTGEAAQDLPFRRSWSVNLDQLLV SAGDQQRLQSVLSSVGSKSTILTLIQEAKAQSENE EDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVH RVFSQGAASQEGTMNRGDFLLSVNGASLAGLAH GNVLKVLHQAQLHKDALVVIKKGMDQPRPSAR QEPPTANGKGLLSRKTIPLEPGIGRSVAVHDALC VEVLKTSAGLGLSLDGGKSSVTGDGPLVIKRVY KGGAAEQAGIIEAGDEILAINGKPLVGLMHFDA WNIMKSVPEGPVQLLIRKHRNSS
3648	A	337	1564	KSRLSVTLMPVQLSEHPEWNESMHSLRISVGGLP VLASMTKAADPRFRPRWKVVLTFFVGAAILWLL CSHRPAPGRPPTHNAHNWRLGQAPANWYNDTY PLSPPQRTPAGIRYRIAVIADLDTESRAQEENTWF TYLKKGYLTFSDSGDKVAVEWDKDHGVLESHL AEKGRGMELSDLIVFNGKLYSVDDRTGVVYQIE GSKAVPWVILSDGDGTVEKGFKAEWLAVKDER LYVGGLGKEWTTTTGDVVNENPEWVKVVGYK GSVDHENWVSNYNALRAAAGIQPPGYLIHESAC WSDTLQRWFFLPRRASQERYSEKDDERKGANLL LSASPDFGDIAVSHVGAVVPTHGFSSFKFIPNTDD QIIVALKSEEDSGRVASYIMAFTLDGRFLLPETKI GSVKYEGIEFI
3649	A	1	775	PTRPGSGSAGGARVGSGEFGVEMAALAPLPPLPA QFKSIQHHLRTAQEHDKRDPVVAYYCRLYAMQ TGMKIDSKTPECRKFLSKLMDQLEALKKQLGDN EAITQEIVGCAHLENYALKMFLYADNEDRAGRF HKNMIKSFYTASLLIDVITVFGELTDENVKHRKY ARWKATYIHNCLKNGETPQAGPVGIEEDNDIEEN EDAGAASLPTQPTQPSSSSTYDPSNMPSGNYTGI QIPPGAHAPANTPAEVPHSTGVAK
3650	A	20	963	KMAATLGPLGSWQQWRRCLSARDGSRRLLLLL LLGSGQGPQQVGAGQTFEYLKREHSLSKPYQGE APRPCFLRDWELQVHFKIHGQGKKNLHGDGLAI WYTKDRMQPGPVFGNMDKFVGLGVFVDTYPNE EKQQERVFPYISAMVNNGSLSYDHERDGRPTEL GGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGK HEWRDCIEVPGVRLPRGYYFGTSSITGDLSDNHD VISLKLFELTVERTPEEEKLHRDVFLPSVDNMKL

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				PEMTAPLPPLSGLALFLIVFFSLVFSVFAIVIGIILY NKWQEQSRKRFY
3651	A	1	1218	RSWAYVKKCKNNMCPNRGLHDGPEPCWLHHA AGTVSAVQARGLQPSQSRSRPRVPGLATALAYG PAHTPPLSRIGWAMQPPPPGPLGDCLRDWEDLQ QDFQNIQVSAAADAGSPPSRVSLAQGGQGSGSPGC KPSLPAEAEGAAQELENQMKERQGLFFDMEAYL PKKNGLYLSLVLGNVNVTLLSKQAKFAYKDEYE KFKLYLTILILISFTCRFLLNSRVTDAAFNFLLVW YYCTLTIRESILINNGSRIKGWWVFHHYVSTFLSG VMLTWPDGLMYQKFRNQFLSFSMYQSFVQFLQ YYYQSGCLYRLRALGERHTMDLTVEGFQSWMW RVLTFLLPFLFFGHFWQLFNALTLFNLAQDPQCK EWQVLMCGFPFLLLFLGNFFTTLRVVHHKFHSQ RHGSKKD
3652	A	640	164	VTTSCIIPFAFGLGVRASERLAEIDMPYLLKYQPM MQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMG DRTSMVQDPGSQAPTSWISESQVFQTTEVLTTRI TELQRRFPTWTPDQYLRGGLCAYSGGAGYVRSS QDLSCDFCNDVLARAKYLKRHGF
3653	A	2	909	IVRRDWQEVSDIHLAMANCKMTKSIRFPALEHC YTGGEVVLPKDQEEWKRRTGLLLYENYGQSETG LICATYWGMKIKPGFMGKATPPYDVQFHMEASV ENCIIVSMNTADPGSQGITHSLLLQVIDDKGSILPP NTEGNIGIRIKPVRPVSLFMCYEGDPEKTAKVEC GDFYNTGDRGKMDEEGYICFLGRSDDIINASGYR IGPAEVESALVEHPAVAESAVVGSPDPIRGEVVK AFIVLTPQFLSHDKDQLTKELQQHVKSVTAPYKY PRKVEFVSELPKTITGKIERKELRKKETGQM
3654	A	2	909	IVRRDWQEVSDIHLAMANCKMTKSIRFPALEHC YTGGEVVLPKDQEEWKRRTGLLLYENYGQSETG LICATYWGMKIKPGFMGKATPPYDVQFHMEASV ENCIIVSMNTADPGSQGITHSLLLQVIDDKGSILPP NTEGNIGIRIKPVRPVSLFMCYEGDPEKTAKVEC GDFYNTGDRGKMDEEGYICFLGRSDDIINASGYR IGPAEVESALVEHPAVAESAVVGSPDPIRGEVVK AFIVLTPQFLSHDKDQLTKELQQHVKSVTAPYKY PRKVEFVSELPKTITGKIERKELRKKETGQM
3655	A	2	2364	SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDTG MVAHINNSRLKAKGVGQHDNAQNFGNQSFEEL RAACLRKGELFEDPLFPAEPSSLGFKDLGPNSKN VQNISWQRPKDIINNPLFIMDGISPTDICQGILGDC WLLAAIGSLTTCPKLLYRVVPRGQSFKKNYAGIF HFQIWQFGQWVNVVVDDRLPTKNDKLVFVHST ERSEFWSALLEKAYAKLSGSYEALSGGSTMEGL EDFTGGVAQSFQLQRPPQNLLRLLRKAVERSSL MGCSIEVTSDSELESMTDKMLVRGHAYSVTGLQ DVHYRGKMETLIRVRNPWGRIEWNGAWSDSAR EWEEVASDIQMQLLHKTEDGEFWMSYQDFLNN FTLLEICNLTPDTLSGDYKSYWHTTFYEGSWRTG SSAGGCRNHPGTFWTNPQFKISLPEGDDPEDDAE GNVVVCTCLVALMQKNWRHARQQGAQLQTIGF VLYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEIF TNSREVSSQLRLPPGEYIIIPSTFEPHRDADFLLRV FTEKHSESWELDEVNYAEQLQEEKVSEDDMDQ

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				DFLHLFKIVAGEGKEIGVYELQRLLNRMAIKFKS FKTKGFGLDACRCMINLMDKDGSGKLGLLEFKI LWKKLKKWMDIFRECDQDHSGTLNSYEMRLVIE KAGIKLNNKVMQVLVARYADDDLIIDFDSFISCF LRLKTMFTFFLTMDPKNTGHICLSLEQVLGEGW EGICRIAPACPSTPPPPSSDVPGPASCPRLFPPWDL LPVSTVAADDHVGIEAL
3656	A	3	174	PLCTHYLLPELPEKSSRTSPRSRPGNMLSGDPHLP QPLCHCLDHCPCCFSGKRLVA
3657	A	1	444	DTRSTYHNAHSLPTYVKSPAPCQMTYIKSPAPCQ TQTCYVQGASPCQSYYVQAPASGSTSQYCVTDP CSAPCSTSYCCLAPRTFGVSPLRRWIQRPQNCNT GSSGCCENSGSSGCCGSGGCGCSCGCGSSGCCCL GIIPMKSRSPALL
3658	A	92	1537	SEAPVQPQPYTMTSFYSTSSCPLGCTMAPGARNV FVSPIDVGCQPVAEANAASMCLLANVAHANRVR VGSTPLGRPSLCLPPTSHTACPLPGTCHIPGNIGIC GAYGKNTLNGHEKETMKFLNDRLANYLEKVRQ LEQENAELETTLLERSKCHESTVCPDYQSYFRTIE ELQQKILCSKAENARLIVQIDNAKLAADDFRIKL ESERSLHQLVEADKCGTQKLLDDATLAKADLEA QQESLKEEQLSLKSNHEQEVKILRSQLGEKFRIEL DIEPTIDLNRVLGEMRAQYEAMVETNHQDVEQ WFQAQSEGISLQAMSCSEELQCCQSEILELRCTV NALEVERQAQHTLKDCLQNSLCEAEDRYGTELA QMQSLISNLEEQLSEIRADLERQNQEYQVLLDVK ARLENEIATYRNLTPLQSLFHACLLYFLSKLWPC HRWVSLWPWSQHGEMILKARVRRLRLVALGSG VPSPCPVFLQD
3659	A	2	402	DLLQCLNQLYSASTEMSCQQSQQQCQPPPKCTP KCPPKCTPKCPPKCPPKCPPQYSAPCPPPVSSCCG SSSGGCCSSEGGGCCLSHHRPRQSLRRRPQSSSC CGSGSGQQSGGSSCCHSSGGSGCCHSSGGCC
3660	A	26	710	CSAVEVKMAARTAFGAVCRRLWQGLGNFSVNT SKGNTAKNGGLLLSTNMKWVQFSNLHVDVPKD LTKPVVTISDEPDILYKRLSVLVKGHDKAVLDSY EYFAVLAAKELGISIKVHEPPRKIERFTLLQSVHI YKKHRVQYEMRTLYRCLELEHLTGSTADVYLEY IQRNLPEGVAMEVTKFCFFIFLDTIRTVTRTHQGA NLGNTIRRKRRKQVIKPQGGHFCLNLK
3661	A	2	370	DVSVAASEPTVYRNPTKMSCQQNQQQCQPPPKC PIPKYPPKCPSKCASSCPPPISSCCGSSSGGCCSSG GCGCCSSEGGGCCLSHHRHHRSHCHRPKSSNCY GSGSGQQSGGSGCCSGGGCC
3662	A	205	1277	RKSLPHPNPQKMLKKPLSAVTWLCIFIVAFVSHP AWLQKLSKHKTPAQPQLKAANCCEEVKELKAQ VANLSSLLSELNKKQERDWVSVVMQVMELESN SKRMESRLTDAESKYSEMNNQIDIMQLQAAQTV TQTSAGKETSPLRERGVPPHLQHCFYIPPDDFLGS PELEVFCDMETSGGGWTIIQRRKSGLVSFYRDW KQYKQGFGSIRGDFWLGNEHIHRLSRQPTRLRVE MEDWEGNLRYAEYSHFVLGNELNSYRLFLGNY TGNVGNDALQYHNNTAFSTKDKDNDNCLDKCA QLRKGGYWYNCCTDSNLNGVYYRLGEHNKHLD GITWYGWHGSTYSLKRVEMKIRPEDFKP

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3663	A	64	1456	LSSAKETLAQMYNTVWNMEDLDLEYAKTDINC GTDLMFYIEMDPPALPPKPPKPTTVANNGMNNN MSLQDAEWYWGDISREEVNEKLRDTADGTFLV RDASTKMHGDYTLTLRKGGNNKLIKIFHRDGKY GFSDPLTFSSVVELINHYRNESLAQYNPKLDVKL LYPVSKYQQDQVVKEDNIEAVGKKLHEYNTQFQ EKSREYDRLYEEYTRTSQEIQMKRTAIEAFNETIK IFEEQCQTQERYSKEYIEKFKREGNEKEIQRIMHN YDKLKSRISEIIDSRRRLEEDLKKQAAEYREIDKR MNSIKPDLIQLRKTRDQYLMWLTQKGVRQKKL NEWLGNENTEDQYSLVEDDEDLPHHDEKTWNV GSSNRNKAENLLRGKRDGTFLVRESSKQGCYAC SVVVDGEVKHCVINKTATGYGFAEPYNLYSSLK ELVLHYQHTSLVQHNDSLNVTLAYPVYAQQRR
3664	A	944	406	GATVEDQSCNFGSLRWVVSVPHISARSCPDPLLS RTGRVPGGRGAGLPRHHSPRCCLQVFFNGANVR QVDVPTLTGAFGILAAHVPTLQVLRPGLVVVHA EDGTTSKYFVSSGSIAVNADSSVQLLAEEAVTLD MLDLGAAKANLEKAQAELVGTADEATRAEIQIR IEANEALVKALE
3665	A	98	1388	ASQLAFGGKLTSTPSRDFQGCGRGAVTCCSFHEH RHQSGRCLSTGMAPNLKGRPRKKKPCPQRRDSF SGVKDSNNNSDGKAVAKVKCEARSALTKPKNN HNCKKVSNEEKPKVAIGEECRADEQAFLVALYK YMKERKTPIERIPYLGFKQINLWTMFQAAQKLG GYETITARRQWKHIYDELGGNPGSTSAATCTRR HYERLILPYERFIKGEEDKPLPPIKPRKQENSSQE NENKTKVSGTKRIKHEIPKSKKEKENAPKPQDAA EVSSEQEKEQETLISQKSIPEPLPAADMKKKIEGY QEFSAKPLASRVDPEKDNETDQGSNSEKVAEEA GEKGPTPPLPSAPLAPEKDSALVPGASKQPLTSPS ALVDSKQESKLCCFTESPESEPQEASFPRLPHHTG HRWQTRMRRRMTNCPPWQITLPTAP
3666	A	113	1492	LLQEMCTKTIPVLWGCFLLWNLYVSSSQTIYPGI KARITQRALDYGVQAGMKMIEQMLKEKKLPDL SGSESLEFLKVDYVNYNFSNIKISAFSFPNTSLAF VPGVGIKALTNHGTANISTDWGFESPLFVLYNSF AEPMEKPILKNLNEMLCPIIASEVKALNANLSTLE VLTKIDNYTLLDYSLISSPEITENYLDLNLKGVFY PLENLTDPPFSPVPFVLPERSNSMLYIGIAEYFFKS ASFAHFTAGVFNVTLSTEEISNHFVQNSQGLGNV LSRIAEIYILSQPFMVRIMATEPPIINLQPGNFTLDI PASIMMLTQPKNSTVETIVSMDFVASTSVGLVIL GQRLVCSLSLNRFRLALPESNRSNIEVLRFENILSS ILHFGVLPLANAKLQQGFPLPNPHKFLFVNSDIEV LEGFLLISTDLKYETSSKQQPSFHVWEGLNLISRQ WRGKSAP
3667	A	1	181	FRGRLGSGRNGGGSMNAPPAFESFLLFEGEKITIN KDTKVPNACLFTINKEDHTLGNIIK
3668	A	212	431	VAGEAVPFFPMMYSEPLKPSYLALVLWYFLLTG YCITKPEVIFKIEQGEEPWILEKGFPSQCHPAKYL WCLHD
3669	A	458	1056	FSGVCFAGIAGSMATLLHDAVMNPAEVVKQRLQ MYNSQHRSAISCIRTVWRTEGLGAFYRSYTTQLT MNIPFQSIHFITYEFLQEQVNPHRTYNPQSHIISGG

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				LAGALAAAATTPLDVCKTLLNTQENVALSLANIS GRLSGMANAFRTVYQLNGLAGYFKGIQARVIYQ MPSTAISWSVYEFFKYFLTKRQLENRAPY
3670	A	145	298	RNPCPLTFLPSTLMVLLLSLTFFSALTFHSICQLRN TGVEVDIVFQRVSFL
3671	A	3	462	ILKVAKKERTMSSLPVPYKLPVSLSVGSCVIIKGT PIHSFINDPQLQVDFYTDMDEDSDIAFRFRVHFG NHVVMNRREFGIWMLEETTDYVPFEDGKQFELC IYVHYNEYEIKVNGHTHLRALSHRIPPSFVEDGC KCPRRYLPWTSVCVCN
3672	A	1	1028	HYAKLGTRPRLKFMSSPSLSDLGKREPAAAADE RGTQQRRACANATWNSIHNGVIAVFQRKGLPDQ ELFSLNEGVRQLLKTELGSFFTEYLQNQLLTKGM VILRDKIRFYEGQKLLDSLAETWDFFFSDVLPML QAIFYPVQGKEPSVRQLALLHFRNAITLSVKLED ALARAHARVPPAIVQMLLVLQGVHESRGVTEDY LRLETLVQKVVSPYLGTYGLHSSEGPFTHSCILEK RLLRRSRSGDVLAKNPVVRSKSYNTPLLNPVQE HEAEGAAAGGTSIRRHSVSEMTSCPEPQGFSDPP GQGPTGTFRSSPAPHSGPCPSRLYPTTQPPEQGLD PTRS
3673	A	2	712	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYF TSSSVNSSAYTIYMGKDKYENEDLIKHGWPEDI WFHVDKLSSAHVYLRLHKGENIEDIPKEVLMDC AHLVKANSIQGCKMNNVNVVYTPWSNLKKTAD MDVGQIGFHRQKDVKIVTVEKKVNEILNRLEKT KVERFPDLAAEKECRDREERNEKKAQIQEMKKR EKEEMKKKREMDELRSYSSLMKVENMSSNQDG NDSDEFM
3674	A	2	712	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYF TSSSVNSSAYTIYMGKDKYENEDLIKHGWPEDI WFHVDKLSSAHVYLRLHKGENIEDIPKEVLMDC AHLVKANSIQGCKMNNVNVVYTPWSNLKKTAD MDVGQIGFHRQKDVKIVTVEKKVNEILNRLEKT KVERFPDLAAEKECRDREERNEKKAQIQEMKKR EKEEMKKKREMDELRSYSSLMKVENMSSNQDG NDSDEFM
3675	A	921	1321	VTLAKMRVHISSCLKVQEQMANCPKFVPVVPTS QPIPSNIPNRSTFACPYCGARNLDQQELVKHCVE SHRSDPNRVVCPICSAMPWGDPSYKSANFLQHL LHRHKFSYDTFVDYSIDEEAAFQAALALSLSEN
3676	A	3	1856	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRR RRMISRYTRKAVPQSLELKGITKHALNHHPPPEK LEEISPTSDSHEKDTSSQSKSDITRESSFTSADTGN SLSAFPSYTGAGISTEGSSDFSWGYGELDQNATE KVQTMFTAIDELLYEQKLSVHTKSLQEECQQWT ASFPHLRILGRQIITPSEGYRLYPRSPSAVSASYET TLSQERDSTIFGIRGKKLHFSSSYAHKASSIAKSSS FCSMERDEEDSIIVSEGIIEEYLAFDHIDIEEGFHG KKSEAATEKQKLGYPPIAPFYCMKEDVLAYVFD SVWCKVVSCMEQLTRSHWEGFASDDESNVAVT RPDSESSCVLSELHPLVLPRVPQSKVLYITSNPMS LCQASRHQPNVNDLLVHGMPLQPRNLSLMDKLL DLDDKLLMRPGSSTILSTRNWPNRAVEFSTSSLS YTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEIL

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				RGARVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVE HVSTVGPQRQMKPHGDSSRAQSAVVDEPNYQQ PQERLLLPDFFPRPNTTQSFLLDTQYRRSCAVEYP HQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P
3677	A	246	757	MRLQGAIFVLLPHLGPILVWLFTRDHMSGWCEG PRMLSWCPFYKVLLLVQTAIYSVVGYASYLVWK DLGGGLGWPLALPLGLYAVQLTISWTVLVLFFT VHNPGLALLHLLLLYGLVVSTALIWHPINKLAAL LLLPYLAWLTVTSALTYHLWRDSLCPVHQPQPT EKSD
3678	A	20	1508	RGKAEFFLAMAGTNALLMLENFIDGKFLPCSSYI DSYDPSTGEVYCRVPNSGKDEIEAAVKAAREAFP SWSSRSPQERSRVLNQVADLLEQSLEEFAQAESK DQGKTLALARTMDIPRSVQNFRFFASSSLHHTSE CTQMDHLGCMHYTVRAPVGVAGLISPWNLPLY LLTWKIAPAMAAGNTVIAKPSELTSVTAWMLCK LLDKAGVPPGVVNIVFGTGPRVGEALVSHPEVPL ISFTGSQPTAERITQLSAPHCKKLSLELGGKNPAII FEDANLDECIPATVRSSFANQGEICLCTSRIFVQK SIYSEFLKRFVEATRKWKVGIPSDPLVSIGALISK AHLEKVRSYVKRALAEGAQIWCGEGVDKLSLPA RNQAGYFMLPTVITDIKDESCCMTEEIFGPVTCV VPFDSEEEVIERANNVKYGLAATVWSSNVGRVH RVAKKLQSGLVWTNCWLIRELNLPFGGMKSSGI GREGAKDSYDFFTEIKTITVKH
3679	A	1862	502	MAGTKPYMEIQTTIREYYEHLYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPITGSEIEAIINSLP TKKIPGPDRFTAKFYQRYKEELSNLIHYLGLSHH LLALNFIIVSFGKKSAWSSAQVKVTDTDFDGVEV RVFEGPPKPEEPLKRSVVYIHGGGWALASAKIRY YDELCTAMAEELNAVIVSIEYRLVPKVYFPEQIH DVVRATKYFLKPEVLQKYMVDPGRICISGDSAG GNLAAALGQQFTQDASLKNKLKLQALIYPVLQA LDFNTPSYQQNVNTPILPRYVMVKYWVDYFKG NYDFVQAMIVNNHTSLDVEEAAAVRARLNWTS LLPASFTKNYKPVVQTTGNARIVQELPQLLDARS APLIADQAVLQLLPKTYILTCEHDVLRDDGIMYA KRLESAGVEVTLDHFEDGFHGCMIFTSWPTNFSV GIRTRNSYIKWLDQNL
3680	A	249	2146	RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFV LFLFLLHRDVSSREEATEKPWLKSLVSRKDHVLD LMLEAMNNLRDSMPKLQIRAPEAQQTLFSINQSC LPGFYTPAELKPFWERPPQDPNAPGADGKAFQK SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSL GPDTRPPECVDQKFRRCPPLATTSVIIVFHNEAWS TLLRTVYSVLHTTPAILLKEIILVDDASTEEHLKE KLEQYVKQLQVVRVVRQEERKGLITARLLGASV AQAEVLTFLDAHCECFHGWLEPLLARIAEDKTV VVSPDIVTIDLNTFEFAKPVQRGRVHSRGNFDWS LTFGWETLPPHEKQRRKDETYPIKSPTFAGGLFSI SKSYFEHIGTYDNQMEIWGGENVEMSFRVWQC GGQLEIIPCSVVGHVFRTKSPHTFPKGTSVIARNQ VRLAEVWMDSYKKIFYRRNLQAAKMAQEKSFG DISERLQLREQLHCHNFSWYLHNVYPEMFVPDL

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				TPTFYGAIKNLGTNQCLDVGENNRGGKPLIMYS CHGLGGNQYFEYTTQRDLRHNIAKQLCLHVSKG ALGLGSCHFTGKNSQVPKDEEWELAQDQLIRNS GSGTCLTSQDKKPAMAPCNPSDPHQLWLFV
3681	A	2982	1869	LKDTLKSQMTQEASDEAEDMKEAMNRMIDELN KQVSELSQLYKEAQAELEDYRKRKSLEDVTAEY IHKAEHEKLMQLTNVSRAKAEDALSEMKSQYSK VLNELTQLKQLVDAQKENSVSITEHLQVITTLRT AAKEMEEKISNLKEHLASKEVEVAKLEKQLLEE KAAMTDAMVPRSSYEKLQSSLESEVSVLASKLK ESVKEKEKVHSEVVQIRSEVSQVKREKENIQTLL KSKEQEVNELLQKFQQAQEELAEMKRYSESSSK LEEDKDKKINEMSKEVTKLKEALNSLSQLSYSTS SSKRQSQQLEALQQQVKQLQNQLAECKKQHQE VISVYRMHLLYAVQGQMDEDVQKVLKQILTMC KNQSQKK
3682	A	447	1024	AQALTAGRQLALAAPFIAPISPISLPRLNPPSQSW NSTPFFKVKLPPQKEVITSDELMAHLGNCLLSIKP QEKSEGLQLNFQQNVDDAMTVLPKLATGLDVN VRFTGVSDFEYTPECSVFDLLGIPLYHGWLVDPQ QSPEAVRAVGKLSYNQL/VGEDHHLQTLQ*HQP RDRKPDCRAVPGDHRGPSDLPRTV
3683	A	2	942	LEIKQEEKFVGQCIKEELMHGECVKEEKDFLKKE IVDDTKVKEEPPINHPVGCKRKLAMSRCETCGTE EAKYRCPRCMRYSCSLPCVKKHKAELTCNGVRD KTAYISIQQFTEMNLLSDYRFLEDVARTADHISR DAFLKRPISNKYMYFMKNRARRQGINLKLLPNG FTKRKENSTFFDKKKQQFCWHVKLQFPQSQA\ST *KKRVPDDKTINEILKPYIDPEKSDPVIRQRLKAYI RSQTGVQILMKIEYMQQNLVRYYELDPYKSLLD NLRNKVIIEYPTLHVVLKGSNNDMKVLHQVKSE STKNVGNEN
3684	A	119	1533	SLQENVQEKRVRVCPGLGGLLPNGTPSITAAAAP QVLWRHVQPGCSHHLHACVIRAACRAGEGHAD RHAGPPET/PVTLPSSWPWSSPWERQCPMH\L*AP GHAFRPVPTEHRRGWAALGHHRAAAGPLREPAS GSQPAPASC*PECHHGCPEQTRQCQDLLREAVV APEQRG*PCAHLQT*ATATTLCPQVPAGRVWQP GHSCHLLPHRHDGSH*HHCAAHRRPVTRRQAAH GVPLPDACYSPHHTLPAAPPPATRPAGHTATHPE *GGDLTPVPDGPHDCPRDVQGIPGAGGGSQLAPC CPPFPAAPVSVQGTQGLGPKNVLH*QWEGIRWQ KEPE/PGPPPEVELKRGAKCRIGDHGLGAVLGQG EYAS*SPSIPW*ASSSACPPLHPTP/TVYTQSPAAA PGWTRPPSP/PPPGLYPGP/PASHAPGVRGGISHQL YSLP*LCRECCSCP/PPPPAHGGRCPSLLPPEALAK LLL
3685	A	101	438	AWVLQCKINTELQTEVVMLKSMVLWLGEQVQS LQLQQQLHCHFNHTHICVTNLEYN\KEYPWDLV KAHLQGASTSNITFDIGELQKK\ILDLNKQTQEFQ PSL*AWTEFQQGLE
3686	A	105	845	VSDVVKNQLVEVQCRQDGCDAVENVHQMFMF NWFTDCLWTLFLSNYQPSVESSSPGGSATSDDHE FDPSADMLVHDFDDERTLEEEEMMEGETNFSSEI EDLAREGDMPIHELLSLYGYGSTVRLPEEDEEE

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				EEEEEGEDDEDADNDDNSGCSGENKEENIKDSS GQEDETQSSNDDPSQSVASQDAQEIIRPRRCKYF DTNSEVEEESEEDEDYIP/SIISFFQSSDGI*SSSSSE DWKKEIMVGS
3687	A	49	1225	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFN HTGELLATGDKGGRVVIFQREPESKNAPHSQGE YDVYSTFQSHEPEFDYLKSLEIEEKINKIKWLPQQ NAAHSLLSTNDKTIKLWKITERDKRPEGYNLKDE EGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFA NGHTYHINSISVNSDCETYMSADDLRINLWHLAI TDRSFTP\NIVDIKPANMEDLTEVITASEFHPHHC NLFVYSSSKGSLRLCDMRAAALCDKHSKLFEEPE DPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYLT VKVWDLNMEARPIETYQVHDYLRSKLCSLYEND CIFDKFECAWNGSDR/IIMTGAYNNFFRMFDRNT KRDVTLEASRGSSKPRAVL
3688	A	1	401	KKVPGRLSEMSFSLNFTLPANTTSSPVT\DCGPSL GLAAGIPLLVATALLVALLFTLIHRRRSSIEAMEE SDRPCEISEIDDNPKISENPRRSPTHEKNTMGAQE AHIYVKTVAGSEEPVHDRYRPTIEMERRR
3689	A	698	889	GRVLVHCAMGVSRSATLVLAFLMIYENMTLVEA IPDGAGPPQISALTQAFVRQLQVLDNRLGRE
3690	A	61	153	MGAHLVRRYLGDASVEPDPLQMPTFPPDYGF
3691	A	61	153	MGAHLVRRYLGDASVEPDPLQMPTFPPDYGF
3692	A	3	2831	PLVRRLLRQTLRRVGGARAVREAVMRAVLTWR DKAEHCINDIAFKPDGTQLILAAGSRLLVYDTSD GTLLQPLKGHKDTVYCVAYAKDGKRFASGSAD KSVIIWTSKLEGILKYTHNDAIQCVSYNPITHQLA SCSSSDFGLWSPEQKSVSKHKSSSKIICCSWTNDG QYLALGMFNGIISIRNKNGEEKVKIERPGGSLSPI WSICWNPSSRWESFWMNRENEDAEDVIVNRYIQ EIPSTLKSAVYSSQGSEAEEEEPEEEDDSPRDDNL EERNDILAVADWG\QKVSFYQLSGKQIGKDRAL NFDPCCISYFTKGEYILLGGSDKQVSLFTKDGVR LGTVGEQNSWVWTGQAKPDSNYVVGGCQDGTI SFYQLIFSTVHGLYKDRYAYRDSMTDVIVQHLIT EQKVRIKCKELVKKIAIYRNRLAIQLPEKILIYELY SEDLSDMHYRVKEKIIKKFECNLLVVCANHIILC QEKRLQCLSFSGVKEREWQMESLIRYIKVIGGPP GREGLLVGLKNGQILKIFVDNLFAIVLLKQATAV RCLDMSASRKKLAVVDENDTCLVYDIDTKELLF QEPNANSVAWNTQCEDMLCFSGGGYLNIKASTF PVHRQKLQGFVVGYNGSKIFCLHVFSISAVEVPQ SAPMYQYLDRKLFKEAYQIACLGVTDTDWRELA MEALEGLDFETAKKERKKRGETNNDLFLADVFS YQGKFHEAAKLYKRSGHENLALEMYTDLCMFE YAKDFLGSGDPKETKMLITKQADWARNIKEPKA AVEMYISAGEHVKAIEICGDHGWVDMLIDIARK LDKAEREPLLLCATYLKKLDSPGYAAETYLKMG DLKSLVQLHVETQRWDEAFALGEKHPEFKDDIY MPYAQWLAENDRFEEAQKAFHKAGRQREAVQV LEQLTNNAVAESRFNDAAYYYWMLSMQCLDIA QDPAQKD
3693	A	3	1099	SSFPTCMRTVFHSNTSVSSLLHRPGHVTPQLTIHG GWRHHRDHTAIDEWDFNPSKFLIYTCLLLFSVLL

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				PLRLDGIIQWSYWAVFAPIWLWKLLVVAGASVG AGVWARNPRYRTEGEACVEFKAMLIAVGIHLLL LMFEVLVCDRVERGTHFWLLVFMPLFFVSPVSV AACVWGFRHDRSLELEILCSVNILQFIFIALKLDRI IHWPWLVVFVPLWILMSFLCLVVLYYIVWSLLFL RSLDVVAEQRRTHVTMAISWITIVVPLLTFEVLL VHRLDGHNTFSYVSIFVPLWLSLLTLMATTFRRK GGNHWWFAIRRDF/CQDQLPQPTGKPPPPPLTDH HGEKALPLQNKDRGSWPASRGSPRLL
3694	A	483	761	PRSLIDYKSYMDTKLLVARFLEQSSCTMTPDIHE LVENIKSVLKSDEEHMEEAITSASFLEQIMAHSX QHIRAHKLPXETAGLXTSELRXLTP
3695	A	483	761	PRSLIDYKSYMDTKLLVARFLEQSSCTMTPDIHE LVENIKSVLKSDEEHMEEAITSASFLEQIMAHSX QHIRAHKLPXETAGLXTSELRXLTP
3696	A	456	733	LSAALWEEPILSLWSETKELTNRGKMNYPQIGPH RPHVKGLRVRPGPGTLSNAPKSLCPGMSNSDRGI H\GGEGQGPGKRAGHLGRGGGMSFL
3697	A	877	1873	VWL*TLS*HTCALMTVCRSCLVKYLEENNTCPT CRIVIHQSHPLQYIGHDRTMQDIVYKLVPGLQEA EMRKQREFYHKLGMEVPGDIKGETCSAKQHLDS HRNGETKADDSSNKEAAE
3698	A	1	572	KQCGIPHEVVRDENSSVYAEVSRLLLATGHWKR LRRDNPRFNLMLGERNRLPFGRLGHEPGLVQLV NYYRGADKLCRKASLVKLIKTSPELAESCTWFPE SYVIYPTNLKTPVAPAQNGIQPPISNSRTDEREFFL ASYNRKKEDGEGNVWIAKSSAGAKVWVQW*M TDLEEEIDIPSPVGLGLESEWPL
3699	A	2008	2432	LHCKMGALETQTHPCSQNMLRSLQKCCCKVEE HHLQPVQVLQTLLHSATAGTGCRRPARPPPAPPT PTPWRSRQSGKQSERAS*LKGRGRYGLGALGGR GGRALGGSRWPPPLPGETLFSGCKHRRRRRGSD AAPGEEAGT
3700	A	33	1318	GYQIGMALASGPARRALAGSGQLGLGGFGAPRR GAYEWGVRSTRKSEPPPLDRVYEIPGLEPITFAG KMHFVPWLARPIFPPWDRGYKDPRFYRSPPLHE HPLYKDQACYIFHHRCRLLEGVKQALWLTKTKL IEGLPEKVLSLVDDPRNHIENQDECVLNVISHARL WQTTEEIPKRETYCPVIVDNLIQLCKSQILKHPSL ARRICVQNSTFSATWNRESLLLQVRGSGGARLST KDPLPTIASREEIEATKNHVLETFYPISPIIDLHECN IYDVKNDTGFQEGYPYPYPHTLYLLDKANLRPH RLQPDQLRAKMILFAFGSALAQARLLYGNDAKV LEQPVVVQSVGTDGRVFHFLVFQLNTTDLDSNE GVKNLAWVDSDQLLYQHFWCLPVIKKRVVVEP VGPVGFKPETFRKFLALYLHGAA
3701	A	86	465	WTLCGPEAGMVGYDPKPDGRNNTKFQVAVAGS VSGLVTRALISPFDVIKIRFQLQHERLSRSDPSAK YHGILQASRQILQEEGPTAFWKGHVPAQILSIGY GAVQFLSFEMLTELVHRGSVYDARE
3702	A	166	814	GFWEKTNQSSHSMDPLGAPSQFVDVDTLPSWGD SCQDELNSSDTTAEIFQEDTVRSPFLYNKDVNGK VVLWKGDVALLNCTAIVNTSNESLTDKNPVSESI FMLAGPDLKEDLQKLKGCRTGEAQLTKGFNLAA RFIIHTVGPKYKSRYRTAAESSLYSCYRNVLQLA

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				KEQSMSSVGFCVINSAKRGYPLKDATHIALRTVR RFLEIHGETIEKVV
3703	A	128	1255	SLGPSPKSATIPCCGDTMAPEEDAGGEALGGSFW EAGNYRRTVQRVEDGHRLCGDLVSCFQERARIE KAYAQQLADWARKWRGTVEKGPQYGTLEKAW HAFFTAAERLSALHLEVREKLQGQDSERVRAWQ RGAFHRPVLGGFRESRAAEDGFRKAQKPWLKRL KEVEASKKSYHAARKDEKTAQTRESHAKADSA VSQEQLRKLQERVERCAKEAEKTKAQYEQTLAE LHRYTPRYMEDMEQAFETCQAAERQRLLFFKD MLLTLHQHLDLSSSEKFHELHRDLHQGIEAASDE EDLRWWRSTHGPGMAMNWPQFEEWSLDTQRTI SRKEKGGRSPDEVTLTSIVPTRDGTAPPPQSPGSP GTGQDEEWSDEESP
3704	A	1	271	ARGEDLALATGGGPDTVTHSNMPCPNSLVYDC WLNIKECSVGEHTFEDLGLCPGRNQREKKRSYK DFLREEEKIAAQVRNSSKKKLKDSE
3705	A	170	1318	LNWANLVIMWPREEEKEKVQDYSLGGLSPDLRI DVSRKKKILKAYDEDEDEDLYPDIHPPPSLPLPG QFTCPQCRKSFTRRSFRPNLQLANMVQIIRQMCP TPYRGNRSNDQGMCFKHQEALKLFCEVDKEAIC VVCRESRSHKQHSVLPLEEVVQEYKAKLQGHVE PLRKHLEAVQKMKAKEERRVTELKSQMKSELA AVASEFGRLTRFLAEEQAGLERRLREMHEAQLG RAGAAASRLAEQAAQLSRLLAEAQERSQQGGLR LLQDIKETFNRCEEVQLQPPEVWSPDPCQPHSHD FLTDAIVRKMSRMFCQAARVDLTLDPDTAHPAL MLSPDRRGVRLAERRQEVADHPKRFSADCCVLG AQGFRSGRHYWEVCMGP
3706	A	204	1996	SRERQTTWMDHNFAPAPPEMQSHGAPGPGTSFS HSHVLGRPIRPSRLPGGGSPLTPVLRKTIHLDTFP QSHIPQTSSRLGLGARTRSVPPQETGIALGASLSP LPTSSLVPRKLSSISLTLHQNSQARSLDRPLSHWE ELPTPGKKAAPHEGGRVSSPGSPPVTLVPGGRVH SEGPGNPGLTKSNRMLATEKPLVSSYLALPFQSR LAQSAPVLAEPGSLGQGHLVSVTDHMPTRASPG KGKPRARGIPRPRGRLQRANTTVNLTAMDTRTD AARHLATMATNRPSLAINLATPNTSQLDTGTEFP ALDIKLGTARDLSSVGTVKSGKTVNLATAGTIKP GTAMNLTTVGTTKPGMVMDLIASEPDKLGKAM ATRSTAKPDMTTEGIAMDSATSDPVKPDTITATV GTSRLETAMALARVNRAKLGTAKNSLALDTSR MGTAVGSVVPVTPDPATGKTTLGSVNNLTISDV ATCLLMPSRSTDLALDNTNAAMDRATEPASLDL ATEYKGKCRNLVGDGLGCREGEVCELGDGSMK PMSINSNLLGYIGIDTIIEQMRKKTMKTGFDFNIM VVGTEGCGAAAGLVAGSTKDPISFPQ
3707	A	3	549	SSSISRDFLGQAACASGTMLRWLRDFVLPTAACQ DAEQPMRYETLFQALDRNGDGVVDIGELQEGLR NLGIPLGQDAEEKIFTTGDVNKDGKLDFEEFMKY LKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQ TLGLTISEQQAELILQSIDVDGTMTVDWNEWRD YFLFNPVTDIEEIIR
3708	A	1	1866	EFRGAGRANMLAPRGAAVLLLHLVLQRWLAAG AQATPQVFDLLPSSSQRLNPGALLPVLTDPALND

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				LYVISTFKLQTKSSATIFGLYSSTDNSKYFEFTVM GRLSKAILRYLKNDGKVHLVVFNNLQLADGRRH RILLRLSNLQRGAGSLELYLDCIQVDSVHNLPRA FAGPSQKPETIELRTFQRKPQDFLEELKLVVRGSL FQVASLQDCFLQQSEPLAATGTGDFNRQFLGQM TQLNQLLGEVKDLLRQEVNETSFLRNTITECQAC GPLKFQSPTPSTVVPPASPAPPTRPPRRCDSNPCF RGVQCTDSRDGFQCGPCPEGYTGNGITCIDVDEC KYHPCYPGEHCINLSPGFRCDACPVGFTGPMVQ GVGISFAKSNKQVCTDIDECRNGACVPNSICVNT LGSYRCGPCKPGYTGDQIRGCKAERNCRNPELN PCSVNAQCIEERQGDVTCVCGVGWAGDGYICGK DVDIDSYPDEELPCSARNCKKDNCKYVPNSGQE DADRDGIGDACDEDADGDGILNEQDNCVLIHNV DQRNSDKDIFGDACDNCLSVLNNDQKDTDGDG RGDACDDDMDGDGIKNILDNCPKFPNRDQRDK DGDGVGDACDSCPDVSNPNQ
3709	A	144	417	TQAMEGLLHYINPAHAISLLSALNEERLKGQLCD VLLIVGDQKFRAHKNVLAASSEYFQSLFTNKENE SQTVFQLDFCEPDAFDNVLNYIY
3710	A	245	688	FGMLKNKGHSSKKDNLAVNAVALQDHILHDLQ LRNLSVADHSKTQVQKKENKSLKRDTKAIIDTGL KKTTQCPKLEDSEKEYVLDPKPPPLTLAQKLGLI GPPPPPLSSDEWEKVKQRSLLQGDSVQPCPICKE EFELRPQVFSIRG
3711	A	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRS TPAMMNGQGSTTSSSKNIAYNCCWDQCQACFNS SPDLADHIRSIHVDGQRGGVFVCLWKGCKVYNT PSTSQSWLQRHMLTHSGDKPFKCVVGGCNASFA SQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSK AGMNKRRKLKNKRRRSLARPHDFFDAQTLDAIR HRAICFNLSAHIESLGKGHSVVFHSTVSILLFFQIK YKTLQKNISTIISKSLKI
3712	A	2	344	RATWHNAGKEREAVQLMAGAEKRVKASHSFLR GLFGGNTRIEEACEMYTRAANMFKMAKNWSAA GNAFCQAAKLHMQLQSKHDSATSFVDAGNAYK KADPQGKTARHVACYLCV
3713	A	20	974	GAAATACSSSSSSSSGAPATWAAHGPGKDVASPS SVSLSPRRSRLLVLRCGLRRNPERPSSSPALRRLL LLLLLLLLLLLGFLLSPGPERGVGGGRFGRRLAL LWAAALGHVVSGKVMSRRAPGSRLSSGGGGGG TNYSRSWNDWQPRTDSASADPGNLKYSSSRDRG GSSSYGLQPSNSAVVSRQRHDDTRVHADIQNDE KGGYSVNGGSGENTYGRKSLGQELRVNNVTSPE FTSVQHGSRALATKDMRKSQERSMSYCDESRLS YLLRRITRENDRDRRLATVKQLKEFIQQPENKLV LVKQLDILAAVHDVLNER
3714	A	237	458	IFALKSPSYLLPCCTPEGKMDHKQLCWSHPQKSG QSSRSCCICSNQHGLIWKYSLNMCLQCCHQYVK DIGFIKL
3715	A	970	1524	LCTLSPGISGTAGSCLTTEPGTELGTSFAQNGFYH EAVVLFTQALKLNPQDHRLFGNRSFCHERLGQP AWALADAQVALTLRPGWPRGLFRLGKALMGLQ RFREAAAVFQETLRGGSQPDAARELRSCLLHLTL QGQRGGICAPPLSPGALQPLPHAELAPSGLPSLRC

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				PRSTALRSPGLSPLLH
3716	A	85	308	QGLPSTMVKLGCSFSGKPGKDPGDQDGAAMDS VPLISPLDISQLQPPLPDQVVIKTQTEYQLSSPDQQ NYTKSR
3717	A	58	618	GAGCTSPGLWARKAAARCLPTYPSRAQPSNVGR RRRRRPGLGALAAGVPAMAESVERLQQRVQELE RELAQERSLQVPRSGDGGGGRVRIEKMSSEVVD SNPYSRLMALKRMGIVSDYEKIRTFAVAIVGVGG VGSVTAEMLTRCGIGKLLLFDYDKVELANMNRL FFQPHQAGLSKVQAAGHTPEE
3718	A	3	593	RGAGGRAGGRADGQPNMADQRQRSLSTSGESL YHVLGLDKNATSDDIKKSYRKLALKYHPDKNPD NPEAADKFKEINNAHAILTDATKRNIYDKYGSLG LYVAEQFGEENVNTYFVLSSWWAKALFVFCGLL TCCYCCCCLCCCFNCCCGKCKPKAPEGEETEFY VSPEDLEAQLQSDEREATDTPIVIQPASATEP
3719	A	2	2173	SGGVRMGSRADGPRTSGHVTGKMAVFPWHSRN RNYKAEFASCRLEAVPLEFGDYHPLKPITVTESK TKKVNRKGSTSSTSSSSSSSVVDPLSSVLDGTDPL SMFAATADPAALAAAMDSSRRKRDRDDNSVVG SDFEPWTNKRGEILARYTTTEKLSINLFMGSEKG KAGTATLAMSEKVRTRLEELDDFEEGSQKELLN LTQQDYVNRIEELNQSLKDAWASDQKVKAPKN VHPGKLVYERIFSMCVDSRSVLPDHFSPENANDT AKETCLNWFFKIASIRELIPRFYVEASILKCNKFLS KTGISECLPRLTCMIRGIGDPL\GSVYARAYL\SRV GMEVAPHLKETLNKNFFDFLLTFKQIHGDTVQN QLVVQGVELPSYLPLYPPAMDWIFQCISYHAPEA LLTEMMERCKKLGNNALLLNSVMSAFRAEFIAT RSMDFIGMIKECDESGFPKHLLFRSLGLNLALAD PPESDRLQILNEAWKVITKLKNPQDYINCAEVWV EYTCKHFTKREVNTVLADVIKHMTPDRAFEDSY PQLQLIIKKVIAHFHDFSVLFSVEKFLPFLDMFQK ESVRVEVCKCI\RTPLSSINKSPPRTRSS*MPFCMF ARPCMTL/CNALTLEDEKRMLSYLINGFIKMVSF GRDFEQQLSFYVESRSMFCNLEPVLVQLIHSVNR LAMETRKVMKGNHSRKTAAFVRSWGAYWFITIP SLAGIFTRLNLYLHSG
3720	A	24	296	ENLFRAGFAFSLLRSSFYISKTYCSWFSNLISGSL ADFNSKGTRDYSPRQMAVRE/KVFDVIIRCFKRH GAEVIDTPVFELKVRNGQEETTW
3721	A	2	310	PSCLTCVGHCSIGGSCTMIGIMMPECHCSLHMTG PRCEEHVFILQQPGHIASILIPLLVLLLLALVAGVV FWHKRRVQGAKGFQHQRMTNGAMNVEIGNPTY K
3722	A	75	722	MELVAGCYEQVLFGFAVHPEPEACGDHEQWTL VADFTHHAHTASLSAVAVNSRFVVTGSKDETJHI YDMKKKIEHGALVHHSGTITCLKFYGNRHLISGA EDGLICIWDAKKWECLKSIKAHKGQVTFLSIHPS GKLALSVGTDKTLRTWNLVEGRSAFIKNIKQNA HIVEWSPRGEQYVVIIQNKIDIYQLDTASISGTITN EKRISSVKFLSES
3723	A	110	316	MELSDNRRSGGLEGLAEKCPNLTYLNLSGNKIK DLSTVEALVSGTVLSLDLLFLVKFSEICLCLLISI
3724	A	3	406	VDRGTEAWQRDPAFSGLQRVGGVDVSFVKGDS

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				VRACASLGVLSFPELEVVYEESRMVSLTAPYVSG FLAFREVPFLLELVQQLREKEPGLMPQVLLVDGN GVLHHRGFGVACHLGVLTDLPCVGVAKKLLQV DG
3725	A	3	406	VDRGTEAWQRDPAFSGLQRVGGVDVSFVKGDS VRACASLGVLSFPELEVVYEESRMVSLTAPYVSG FLAFREVPFLLELVQQLREKEPGLMPQVLLVDGN GVLHHRGFGVACHLGVLTDLPCVGVAKKLLQV DG
3726	A	.1	433	SSDDRSLFRRLKLNYAIFDEGHMLKNMGSIRYQ HLMTINANNRLLLTGTPVQNNLLELMSLLNFVM PHMFSSSTSEIRRMFSSKTKSADEQSIYEKERIAH AKQIIKPFILRRVKEEVLKQLPPKKDRIELCAMSE KQEQLYLG
3727	A	6	383	RIPRGKACXTVLGRSTGELEGFASSRLPPQPCGW GQSSDLLSRIDLDELMKKDEPPLDFPDTLEGFEY AFNEKGQLRHIKTGEPFVFNYREHLHRWNQKRY EALGEIITKYVYELLEKDCNSKKVS
3728	A	3	2452	EIAGAAAENMLGSLLCLPGSGSVLLDPCTGSTISE TTSEAWSVEVLPSDSEAPDLKQEERLQELESCSG LGSTSDDTDVREVSSRPSTPGLSVVSGISATSEDIP NKIEDLRSECSSDFGGKDSVTSPDMDEITHDFLYI LQPKQHFQHIEAEADMRIQLSSSAHQLTSPPSQSE SLLAMFDPLSSHEGASAVVRPKVHYARPSHPPPD PPILEGAVGGNEARLPNFGSPMF*LPAEMEAFKQ RHS/YTPERLVRSRSS\DIVSSVRRPMSDPSWNRR P\GNEERELPPAAAIGATSLVAAPHSSSSSPSKDSS RGETEERKDSDDEKSDRNRPWWRKRFVSAMPK APIPFRKKEKQEKDKDDLGPDRFSTLTDDPSPRLS AQAQVAEDILDKYRNAIKRTSPSDGAMANYEST EVMGDGESAHDSPRDEALQNISADDLPDSASQA AHPQDSAFSYRDAKKKLRLALCSADSVAFPVLT\ HSTRNGLPDHTDPEDNEIVCFLKVQIAEAINLQD KNLMAQLQETMRCVCRFDNRTCRKLLASIAEDY RKRAPYIAYLTRCRQGLQTTQAHLERLLQRVLR DKEVANRYFTTVCVRLLLESKEKKIREFIQDFQK LTAADDKTAQVEDFLQFLYGAMAQDVIWQNAS EEQLQDAQLAIERSVMNRIFKLAFYPNQDGDILR DQVLHEHIQRLSKVVTANHRALQIPEVYLREAP WPSAQSEIRTISAYKTPRDKVQCILRMCSTIMNLL SLANEDSVPGADDFVPVLVFVLIKANPPCLLSTV QYISSFYASCLSGEESYWWMQFTAAVEFIKTIDD RK
3729	A	3	2452	EIAGAAAENMLGSLLCLPGSGSVLLDPCTGSTISE TTSEAWSVEVLPSDSEAPDLKQEERLQELESCSG LGSTSDDTDVREVSSRPSTPGLSVVSGISATSEDIP NKIEDLRSECSSDFGGKDSVTSPDMDEITHDFLYI LQPKQHFQHIEAEADMRIQLSSSAHQLTSPPSQSE SLLAMFDPLSSHEGASAVVRPKVHYARPSHPPPD PPILEGAVGGNEARLPNFGSPMF*LPAEMEAFKQ RHS/YTPERLVRSRSS\DIVSSVRRPMSDPSWNRR P\GNEERELPPAAAIGATSLVAAPHSSSSSPSKDSS RGETEERKDSDDEKSDRNRPWWRKRFVSAMPK APIPFRKKEKQEKDKDDLGPDRFSTLTDDPSPRLS AQAQVAEDILDKYRNAIKRTSPSDGAMANYEST

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				EVMGDGESAHDSPRDEALQNISADDLPDSASQA AHPQDSAFSYRDAKKKLRLALCSADSVAFPVLT\ HSTRNGLPDHTDPEDNEIVCFLKVQIAEAINLQD KNLMAQLQETMRCVCRFDNRTCRKLLASIAEDY RKRAPYIAYLTRCRQGLQTTQAHLERLLQRVLR DKEVANRYFTTVCVRLLLESKEKKIREFIQDFQK LTAADDKTAQVEDFLQFLYGAMAQDVIWQNAS EEQLQDAQLAIERSVMNRIFKLAFYPNQDGDILR DQVLHEHIQRLSKVVTANHRALQIPEVYLREAP WPSAQSEIRTISAYKTPRDKVQCILRMCSTIMNLL SLANEDSVPGADDFVPVLVFVLIKANPPCLLSTV QYISSFYASCLSGEESYWWMQFTAAVEFIKTIDD RK
3730	A	3	2452	EIAGAAAENMLGSLLCLPGSGSVLLDPCTGSTISE TTSEAWSVEVLPSDSEAPDLKQEERLQELESCSG LGSTSDDTDVREVSSRPSTPGLSVVSGISATSEDIP NKIEDLRSECSSDFGGKDSVTSPDMDEITHDFLYI LQPKQHFQHIEAEADMRIQLSSSAHQLTSPPSQSE SLLAMFDPLSSHEGASAVVRPKVHYARPSHPPPD PPILEGAVGGNEARLPNFGSPMF*LPAEMEAFKQ RHS/YTPERLVRSRSS\DIVSSVRRPMSDPSWNRR P\GNEERELPPAAAIGATSLVAAPHSSSSSPSKDSS RGETEERKDSDDEKSDRNRPWWRKRFVSAMPK APIPFRKKEKQEKDKDDLGPDRFSTLTDDPSPRLS AQAQVAEDILDKYRNAIKRTSPSDGAMANYEST EVMGDGESAHDSPRDEALQNISADDLPDSASQA AHPQDSAFSYRDAKKKLRLALCSADSVAFPVLT\ HSTRNGLPDHTDPEDNEIVCFLKVQIAEAINLQD KNLMAQLQETMRCVCRFDNRTCRKLLASIAEDY RKRAPYIAYLTRCRQGLQTTQAHLERLLQRVLR DKEVANRYFTTVCVRLLLESKEKKIREFIQDFQK LTAADDKTAQVEDFLQFLYGAMAQDVIWQNAS EEQLQDAQLAIERSVMNRIFKLAFYPNQDGDILR DQVLHEHIQRLSKVVTANHRALQIPEVYLREAP WPSAQSEIRTISAYKTPRDKVQCILRMCSTIMNLL SLANEDSVPGADDFVPVLVFVLIKANPPCLLSTV QYISSFYASCLSGEESYWWMQFTAAVEFIKTIDD RK
3731	A	1	1305	VNTAMHEAKLMEECDELVEIIQQRKQMIAVKIK ETKVMKLRKLAQQVANCRQCLERSTVLINQAEH ILKENDQARFLQSAKNIAERVAMATASSQVLIPDI NFNDAFENFALDFSREKKLLEGLDYLTAPNPPSIR EELCTASHDTITVHWISDDEFSISSYELQYTIFTGQ ANFISLYNSVDSWMIVPNIKQNHYTVHGLQSGTR YIFIVKAINQAGSRNSEPTRLKTNSQPFKLDPKMT HKKLKISNDGLQMEKDESSLKKSHTPERFSGTGC YVYGVLHNSDNS*MFISLSFPLSHRYAIGIAYKSA PKNEWIGKNASSWVFSRCNSNFVVRHNNKEML VDVPPHLKRLGVLLDYDNY/NMLSFYDPANSL\H LHTFDVTF\ILPVCPTFTIWNKSLMILSGLPAPDFI DYPERQECNCRPQESPYVSGMKTCH
3732	A	127	2832	LGQRLSLVPRPSLKRRLGKRLSLGLRERMMSLW WS/GPKVRTQATTGARPKTETKSVPAARPKTEAQ AMSGARPKTEVQVMGGARPKTEAQGITGARPKT DARAVGGARSKTDAKAIPGARPKDEAQAWAQS

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				EFGTEAVSQAEGVSQTNAVAWPLATAESGSVTK SK\ACLWIEN*SMWM/PETFPGTQGQKGIQPWFG PGEETNMGSWCYSRPRAREEASNESGFWSADET STASSFWTGEETSVRSWPREESNTRSRHRAKHQT NPRSRPRSKQEAYVDSWSGSEDEASNPFSFWVG ENTNNLFRPRVREEANIRSKLRTNREDCFESESED EFYKQSWVLPGEEAN\IDSGTETKKILILPWKLRA QKDVDSDRVKQEPRFEEEVIIGSWFWAEKEASLE GGASAICESEPGTEEGAIGGSAYWAEEKSSLGAV AREEAKPESEEEAIFGSWFWDRDEACFDLNPCPV YKVSDRFRDAAEELNASSRPQTWDEVTVEFKPG LFHGVGFRSTSPFGIPEEASEMLEAKPKNLELSPE GEEQESLLQPDQPSPEFTFQYDPSYRSVREIREHL RARESAESESWSCSCIQCELKIGSEEFEEFLLLMD KIRDPFIHEISKIAMGMRSASQFTRDFIRDSGVVS LIETLLNYPSSRVRTSFLENMIHMAPPYPNLNMIE TFICQVCEETLAHSVDSLEQLTGNKGCFRHLTMT IDYHT\LIAN*YGPGFPLLF*PQAQCGETKFHVLK MLLNLSENPAVAKKLFSAKALSIFVGLFNIEETN DNIQIVIKMFQNISNIIKSGKMSLIDDDFSLEPLISA FREFEELAKQLQAQIDNQNDPEATGTTAFVGKG NNPSANRERLSPSVFCPGAQEAESLPARRVRGEE QRLLLEEVGARTADGIPEGW
3733	A	2	3274	DVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHC FYEVEVAILPDEIFRLVKIRFLIEDINDNAPLFPAT VINISIPENSAINSKYTLPAAVDPDVGINGVQNYE LIKSQNIFGLDVIETPGGDKMPQLIVQKELDREEK DTYVMKVKVEDGGFPQRSSTAILQVSVTDTNDN HPVFKETEIEVSIPENAPVGTSVTQLHATDADIGE NAKIHFSFSNLVSNIARRLFHLNATTGLITIKEPLD REETPNHKLLVLASDGGLMPARAMVLVNVTDV NDNVPSIDIRYIVNPVNDTVVLSENIPLNTKIALIT VTDKDADHNGRVTCFTDHEIPFRLRPVFSNQFLL ETAAYLDYESTKEYAIKLLA\ADAGKPPLNQSAM LFIKVKDENDNAPVFTQSFVTVSIPENNSPGIQLT KVSAMDADSGPNAKINYLLGPDAPPEFSLDCRT GMLTVVKKLDREKEDKYLFTILAKDNGVPPLTS NVTVFVSIIDQNDNSPVFTHNEYNFYVPENLPRH GTVGLITVTDPDYGDNSAVTLSILDENDDFTIDSQ TGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSS AKVTINVVDVNDNKPVFIVPPSNCSYELVLPSTN PGTVVFQVIAVDNDTGMNAEVRYSIVGGNTRDL FAIDQETGNITLMEKCDVTDLGLHRVLVKANDL GQPDSLFSVVIVNLFVNESVTNATLINELVPQKH LKHQ*PQILEIADVSSPTSDYVKILVAAVAGTITV VVVIFITAVVRCRQAPHLKAAQKNMQNSEWATP NPENRQMIMMKKKKKKKKHSPKNLLLNVVTIEE TKADDVDSDGNRVTLDLPIDLEEQTMGKYNWV TTPTTFKPDSPDLARHYKSASPQPAFQIQPETPLN LKHHIIQELPLDNTFVACDSISNCSSSSSDPYSVSD CGYPVTTFEVPVSVHTRPPVDLEVGGAQSGQVAI LTSSLMELLLCLMVAAFLPLELRPLGQQNVMSW EQEAKILLVGYWGDGEWCHFHFHHLIPGPVNPG YERKQYHILDSDSEDTQPSGELCPIPVRPFTILSIQ LLQDDGEHCGTKQGFQPAVQLGLLPHKTLK

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3734	A	1	840	GTRPGHLPAPSDGFCV/HL*SIPSWGSF*GESL/EM QLITSLGLQEFDIARNVLELIYAQTLVWIGIFFCPL LPFIQMIMLFIMFYSKNISLMMNFQPPSKAWRAS QMMTFFIFLLFFPSFTGVLCTLAITIWRLKPSADC GPFRGLPLFIHSIYSWIDTLSTRPGYLWVVWIYRN LIGSVHFFFILTLIVLIITYLYWQITEGRKIMIRLLH EQIINEGKDKMFLIEKLIKLQDMEKKANPSSLVLE RREVEQQGFLHLGEHDGSLDLRSRRSVQEGNPR A
3735	A	2	432	VEVCRRYLWKMTVDASQNVQCCVIFSHFPFIFN NLSKIKLLHTDTLLKIESKKHKAYLRSAAIEEERE SEFALRPTFDLTVRRNHLIEDVLNQLSQFENEDL RKELWVSFSGEIGYDLGGS/VKKEIFYCLFAEMIQ PEYGMFMY
3736	A	1542	343	KGAPSFVRLYQYPNFAGPHAALANKSFFKADKV TMLWNKKATAVLVIASTDVDKTGASYYGEQTL HYIATNGESAVVQLPKNGPIYDVVWNSSSTEFCA VYGFMPAKATIFNLKCDPVFDFGTGPRNAAYYS PHGHILVLAGFGNLILQI*AD/IMKVWNVKNYKLI SKPVASDSTYFAWCPDGEHILTATCAPRLRVNN GYKIWHYTGSILHKYDVPSNAELWQVSWQPFLD GIFPAKTITYQAVPSEVPNEEPKVATAYRPPALRN KPITNSKLHEEEPPQNMKPQSGNDKPLSKTALKN QRKHEAKKAAKQEARSDKSPDLAPTPAPQSTPR NTVSQSISGDPEIDKKIKNLKKKLKAIEQLKEQAA TGKQLEKNQLEKIQKETALLQELEDLELGI
3737	A	3190	664	VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPLKEE EILPEPGSETPTVASEALAELLHGALLRRGPEMG YLPGPPLGPEGGEEETTTTIITTTTVTTTVTSPVLC NNNISEGEGYVESPDLGSPVSRTLGLLDCTYSIHV YPGYGIEIQVQTLNLSQEEELLVLAGGGSPGLAP RLLANSSMLGEGQVLRSPTNRLLLHFQSPRVPRG GGFRIHYQAYLLSCGFPPRPAHGDVSVTDLHPGG TATFHCDSGYQLQGEETLICLNGTRPSWNGETPS CMASCGGTIHNATLGRIVSPEPGGAVGPNLTCR WVIEAAEGRRLHLHFERVSLDEDNDRLMVRSGG SPLSPVIYDSDMDDVPERGLISDAQSLYVELLSET PANPLLLSLRFEAFEEDRCFAPFLAHGNVTTTDPE YRPGALATFSCLPGYALEPPGPPNAIECVDPTEPH WNDTEPACKAMCGGELSEPAGVVLSPDWPQSY SPGQDCVWGVHVQEEKRILLQVEILNVREGDML TLFDGDGPSARVLAQLRGPQPRRRLLSSGPDLTL QFQAPPGPPNPGLGQGFVLHFKEVPRNDTCPELP PPEWGWRTASHGDLIRGTVLTYQCEPGYELLGS DILTCQWDLSWSAAPPACQKIMTCADPGEIANG HRTASDAGFPVGSHVQYRCLPGYSLEGAAMLTC YSRDTGTPKWSDRVPKCALKYEPCLNPGVPENG YQTLYKHHYQAGESLRFFCYEGFELIGEVTITCV PGHPSQWTSQPPLCKVTQTTDPSRQLEGGNLAL AILLPLGLVIVLGSGVYIYYTKLQGKSLFGFSGSH SYSPITVESDFSNPLYEAGDTREYEVSI
3738	A	3190	664	VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPLKEE EILPEPGSETPTVASEALAELLHGALLRRGPEMG YLPGPPLGPEGGEEETTTTIITTTTVTTTVTSPVLC NNNISEGEGYVESPDLGSPVSRTLGLLDCTYSIHV

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				YPGYGIEIQVQTLNLSQEEELLVLAGGGSPGLAP RLLANSSMLGEGQVLRSPTNRLLLHFQSPRVPRG GGFRIHYQAYLLSCGFPPRPAHGDVSVTDLHPGG TATFHCDSGYQLQGEETLICLNGTRPSWNGETPS CMASCGGTIHNATLGRIVSPEPGGAVGPNLTCR WVIEAAEGRRLHLHFERVSLDEDNDRLMVRSGG SPLSPVIYDSDMDDVPERGLISDAQSLYVELLSET PANPLLLSLRFEAFEEDRCFAPFLAHGNVTTTDPE YRPGALATFSCLPGYALEPPGPPNAIECVDPTEPH WNDTEPACKAMCGGELSEPAGVVLSPDWPQSY SPGQDCVWGVHVQEEKRILLQVEILNVREGDML TLFDGDGPSARVLAQLRGPQPRRRLLSSGPDLTL QFQAPPGPPNPGLGQGFVLHFKEVPRNDTCPELP PPEWGWRTASHGDLIRGTVLTYQCEPGYELLGS DILTCQWDLSWSAAPPACQKIMTCADPGEIANG HRTASDAGFPVGSHVQYRCLPGYSLEGAAMLTC YSRDTGTPKWSDRVPKCALKYEPCLNPGVPENG YQTLYKHHYQAGESLRFFCYEGFELIGEVTITCV PGHPSQWTSQPPLCKVTQTTDPSRQLEGGNLAL AILLPLGLVIVLGSGVYIYYTKLQGKSLFGFSGSH SYSPITVESDFSNPLYEAGDTREYEVSI
3739	A	734	445	LLEPEPAEEYTEQSEVEST/EGMILI*CCLYFAAFQ TNVSNIYFALQYVNRQFMAETQFTSGEKEQVDE WTVETVEVRVLCIAKLLSLSSVSNFYLY
3740	A	2	1578	MAHYITFLCMVLVLLLQNSVLAEDGEVRSSCRT APTDLVFILDGSYSVGPENFEIVKKWLVNITKNF DIGPKFIQVGVVQYSDYPVLEIPLGSYDSGEHLTA AVESILYLGGNTKTGKAIQFALDYLFAKSSRFLT KIAVVLTDGKSQDDVKDAAQAARDSKITLFAIG VGSETEDAELRAIANKPSSTYVFYVEDYIAISKIR EVMKQKLCEESVCPTRIPVAARDERGFDILLGLD VNKKVKKRIQLSPKKIKGYEVTSKVDLSELTSNV FPEGLPPSYVFVSTQRFKVKKIWDLWRILTIDG/* PQIAVTLNGVDKILLFTTTSVINGSQVVTFANPQV KTLFDEGWHQIRLLVTEQDVTLYIDDQQIENKPL HPVLGILINGQTQIGKYSGKEETVQFDVQKLRIY CDPEQNNRETACEIPGFCLNGPSDVGSTPAPCICP PGKPGLQGPKGDPGLPGNPGYPGQPGQDGKPVS TESLVISGISGITGYQGIAGTPGVPGSPGIQGARGL. PGYKGEPGRDGDK
3741	A	5048	1236	MSAPAGSSHPAASARIPPKFGGSAVSGAAAPAGP GAGPAPHQQNGPAQNQMQVPSGYGLHHQNYIA PSGHYSQGPGKMTSLPLDTQCGDYYSALYTVPT QNVTPNTVNQQPGAQQLYSRGPPAPHIVGSTLGS FQGAASSASHLHTSASQPYSSFVNHYNSPAMYS ASSSVASQGFPSTCGHYAMSTVSNAAYPSVSYPS LPAGDTYGQMFTSQNAPTVRPVKDNSFSGQNTA ISHPSPLPPLPSQQHHQQQSLSGYSTLTWSSPGLP STQDNLIRNHTGSLAVANNNPTITVADSLSCPVM QNVQPPKSSPVVSTVLSGSSGSSSTRTPPTANHPV EPVTSVTQPSELLQQKGVQYGEYVNNQASSAPT PLSSTSDDEEEEEEDEEAGVDSSSTTSSASPMPNS YDALEGGSYPDMLSSSASSPAPDPAPEPDPASAP APASAPAPVVPQPSKMAKPLAMAIQHFSLVIRML QHHLFLEYSPSNPVYSGFQQYPQQYPGVNQLSSS

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				IGGLSLQSSPQPESLRPVNLTQERNILPMTPVWAP VPNLNADLKKLNCSPDSFRCTLTNIPQTQALLNK AKLPLGLLLHPFRDLTQLPVITSNTIVRCRSCRTYI NP\FVSFIDQRR*KCNLCYRVNDVPEEFMYNPLT RSYGEPHKRPEVQNS\TVEFIASSDYMLRPPQPAV YLFVLDVSHNAVEAGYLTI/LWCQSLLE\NLDKLP G\DSRT\RIGFMTFD\STYSFLQFTQEGLSQPQMLI VSDIDDVFLPTPDSLLVNLYESKELIKDLLNALPN MFTNTRETHSALGPALQAAFKLMSPTGGRVSVF QTQLPSLGAGLLQSREDPNQRSSTKVVQHLGPAT DFYKKLALDCSGQQTAVDLFLLSSQYSDLASLA CMSKYSAGCIYYYPSFHYTHNPSQAEKLQKDLK RYLTRKIGFEAVMRIRCTKGLSMHTFHGNFFVRS TDLLSLANINPDAGFAVQLSIEESLTDTSLVCFQT ALLYTSSKGERRIRVHTLCLPVVSSLSDVYAGVD VQAAICLLANMAVDRSVSSSLSDARDALVNAVV DSLSAYGSTVSNLQHSALMAPSSLKLFPLYVLAL LKQKAFRTGTSTRLDDRVYAMCQIKSQPLVHLM KMIHPNLYRIDRLTDEGAVHVNDRIVPQPPLQKL SAEKLTREGAFLMDCGSVFYIWVGKGCDNNFIE DVLGYTNFASIPQKMTHLPELDTLSSERARSFIT WLRDSRPLSPILHIVKDESPAKAEFFQHLIEDRTE AAFSYYEFLLHVQQQICK
3742	A	934	68	SMLASQGVLLHPYGVPMIVPAAPYLPGLIQGNQE AAAAPDTMAQPYASAQFAPPQNGIPAEYTAPHP HPAPEYTGQTTVPEHTLNLYPPAQTHSEQSPADT SAQTVSGTRNKQD*RSTDGWPSPKTQTS*KHGK QVSSPSGLHVSNIPFR\FRDPDLRQMF\GQFGKILD VEIIFNERGSKGFGFVTFENSADADRAREK\LHGT VV\EGRKI\EVN\NATARVMTNKKTVNPYTNGWK LNPVVGAVYSPEFYAGTVLLCQANQEGSSMYSA PSTDFRGAKLHTSRPLLSGS
3743	A	3	1456	QFQQAWMQNKVPIPAPNEVLNDRKEDIKLEEKK KTQAEIEQEMATLQYTNPQLLEQLKIERLAQKQV EQIQPPPSSGTPLLGPQPFPGQGPMSQIPQGF/PTA PSISADANEHGS\KGPPGPQGQFRPPGPQGQMGP QGPPLHQGGGGPQGFMGPQGPQGPPQGLPRPQD MHGPQGMQRHPGPHGPLGPQGPPGPQGSSGPQG HMGPQGPPGPQGHIGPQGPPGPQGHLGPQGPPGT QGMQGPPGPRGMQGPPHPHGIQGGPGSQGIQGP VSQGPLMGLNPKGMQGPPGPRENQGPAPQGMI MGHPPQEMRGPHPPGGLLGHGPQEMRGPQEIRG MQGPPPQGSMLGPPQELRGPPGSQSQQGPPQGSL GPPPQGGMQGPPGPQGQQNPARGPHPSQGPIPFQ QQKTPLLGDGPRAPFNQEGQSTGPPPLIPGLGQQ GAQGRIPPLNPGQGPGPNKVS/ERGAPPRHEGRA PPRGRDGFPGPMKTLV
3744	A	1571	652	PLTGRKCPGWTHSGSRRSPRIAEEVPGFPKRAEA SRQFSETADRLELLRRAVMAAARATTPADGEEP APEAEALAAARERSSRFLSGLELVKQGAEARVFR GRFQGRÅAVIKHRFPKGYRHPALEARLGRRRTV QEARALLRCRRAGISAPVVFFVDYASNCLYMEEI EGSVTVRD\IFSPLWRLKKTPQGLSNLAKTIGQVL ARMHDEDLIHGDLTTSNMLLKPPLEQLNIVLIDF GLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFE

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				AFLKSYSTSSKKARPVLKKLDEVRLRGKKRSMV G
3745	A	127	1433	GSHRFSLASPLDPEVGPYCDTPTMRTLFNLLWLA LACSPVHTTLSKSDAKKAASKTLLEKSQFSDKPV QDRGLVVTDLKAESVVLEHRSYCSAKARDRHFA GDVLGYVTPWNSHGYDVTKVFGSKFTQISPVWL QLKRRGREMFEVTGLHDVDQGWMRAVRKHAK GL\P*CLGSCLRTGLTMISG/YVLDSEDEIEELSKT VVQVAKNQHFDGFVVEVWNQLLSQKRVGLIHM LTHLAEALHQARLLALLVIPPAITPGTDQLGMFT HKEFEQLAPVLDGFSLMTYDYSTAHQPGPNAPL SWVRACVQVLDPKSKWRSKILLGLNFYGMDYA TSKDAREPVVGARYIQTLKDHRPRMVWDSQVSE HFFEYKKSRSGRHVVFYPTLKSLQVRLELARELG VGVSIWELGQGLDYFYDLL*VGIAASAVDVFFSK PWSE
3746	A	1	898	IDRAAECRTKPLPMAVSIRGNADSIVACLVLMVL YLIKKRLVACAAVFYGFAVHMKIYPETYILPITL HLLPDRDNDKSLRQFRYTFQACL*ELLKRLCNRT ALMFVAVAGLTFFALSFGFYYEYGWEFLEHTYF YHLTRRDIRHNFSPYFYMLYLTAESKWSFSLGIA AFLPQLILLSAVSFAYYRDLVFCWFLHTSIFVTFN KVCTSQYFLWYLCLLPLVMPLVRMPWKRAVVL LMLWFIGQAMWLAPAYVLEFQGKNTFLFIWLA GLFFLLINCSILIQIISHYKEEPLTERIKYD
3747	A	1	2325	MVISFQGLVTFGDVAVDFSQEEWEWLNPIQRNL YRKVMLENYRNLASLGLCVSKPDVISSLEQGKEP WTVKRKMTRAWCPDLKAVWKIKELPLKKDFCE GKLSQAVITERLTSYNLEYSLLGEHWDYDALFET QPGLVTIKNLAVDFRQQLHPAQKNFCKNGIWEN NSDLGSAGHCVAKPDLVSLLEQEKEPWMVKREL TGSLFSGQRSVHETQELFPKQDSYAEGVTDRTSN TKLDCSSFRENWDSDYVFGRKLAVGQETQFRQE PITHNKTLSKERERTYNKSGRWFYLDDSEEKVH NRDSIKNFQKSSVVIKQTGIYAGKKLFKCNECKK TFTQSSSLTVHQRIHTGEKPYKCNECGKAFSDGS SFARHQRCHTGKKPYECIECGKAFIQNTSLIRHW RYYHTGEKPFDCIDCGKAFSDHIGLNQHRRIHTG EKPYKCDVCHKSF\RYGSSLTVHQRIHTGEKPYE CDVCRKAFSHHASLT\Q\HQRVHSGEKPFKCKEC GKAFRQNIHLASHLRIHTGEKPFECAECGKSFSIS SQLATHQRIHTGEKPYECKVCSKAFTQKAHLAQ HQKTHTGEKPYECKECGKAFSQTTHLIQHQRVH TGEKPYKCMECGKAFGDNSSCTQHQRLHTGQRP YECIECGKAFKTKSSLICHRRSHTGEKPYECSVC GKAFSHRQSLSVHQRIHSGKKPYECKECRKTFIQI GHLNQHKRVHTGERSYNYKKSRKVFRQTAHLA HHQRIHTGESSTCPSLPSTSNPVDLFPKFLWNPSS LPSP
3748	A	823	1	GGYTKSGYDSACKDFVPHDLEVQIPGRVFLVTG GNSGIGKATALEIAKRGGTVHLVCRDQAPAEDA RGEIIRE\SGNQNIFLHIVDLSDPKKIWKFVENFKQ EHKLHVL\VNNAGCMVNKREAHKKMDFEKNFG CQYSGVCTFLTTRPDPLCWRKNTDPRVIT\VSSG GMLVQKLNNQ*SPVRKNTIWMGTMVYAQNKVS

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				ERQQVVLT\ERWGPRAPG\IHFSSMHPGWA\DTPG VRQAMPGFHVQASGYRLRSEAQGADTMLWLAL SSARSRTAQRP
3749	A	1939	715	GFLRLSQAT\RQRLSIPVMVLTLDPTRD\QCFGDR FSRLLLDEFLGYDDIL\MSSVKGLAENEENKGFLR NVVSGEHYRFV\SMWMART\SYLAAFANHGQSF TLSVSHACCGYSHHQIFVFIVDLLQMLEMNMAIA FPAAPLLTVILALVGMEAIMSEFFNDTTTAFYIILI VWLADQYDAICCHTSTSKRHWLRFFYLYHFAFY AYHYRFNGQYSSLALVTSWLFIQHSMIYFFHHYE LPAILQHVRIQ\EMLLQAPTLGPGTPTA\LPDDMN NNSGAPATAP\DSAGQPPALGPVSPGASGSPGPV AAAPSSLVAAAASVAAAAGGDLGWMAETAAIIT DASFLSGLSASLLERRPASPLGPAGGLPHAPQDS VPPSDSAASDTTPLGAAVGGPSPASMAPTEAPSE VGS
3750	A	2	844	GLLEPFSKLLSFVIQNAVFTLAYLVELCGLCYRA FTKERDKFYLSRSVVLELLQALKLKSPLPDTNLL LLVQFICADAGTKLAESTILSKQMIASVPGCGTA AMECVRQYINEVLDFM\ADMHTLTKLKSHMKTC SQPLHEDTFGGHLKVGLAQIAAMDISRGNHRDN KAVIRYLPWLYHPPSAMQQGPKEFIECVSHIRLL SWLLLGSLTHNAVC/LKWPPLPGLPIPLDAGSHV ADHLIVILIGFPEQSKTSVL\HMCSLFHAF\SLAQL WDSLLARQSGRW
3751	A	431	2	AFTRKCEETAFIVPQCEIIPTE/WVCRRIPTGSSLER NPGVKEGCEFCPPKVEMFFKDDANHDPQWSRQ QLIAAKFGFAALGI/QTEVDIMSHAT*AVFEIPEKS RL\PQNCTPVDMKIEFGVHVTSKEILTDVIDNDS* RHSPS
3752	A	131	1278	AWSGSGLLVLCINTASMPMISVLGKMFLWQREG PGGRWTCQTSRRVSSDPAWAVEWIELPRGLSLSS LGSARTLRGWSRSSRPSSVDSQDLPEVNVGDTV AMLPKSRRALTIQEIAALARSSLHGISQVVKDHV TKPTAMAQGRVAHLIEWKGWSKPSDSPAALESA FSSYSDLSEGEQEARFAAGVAEQFAIAEAKLRA WSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPL GPHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSP DTLCSSLCSLEDGLLGSPARLA\PSCWAMSCFSPN CPPAGKVPSAAW/APLEAQDSLYNSPLTESCLSP AEEEPAPCKDCQPLCPPLTGSWERQRQASDLASS GVVSLDEDEAEPEEQ
3753	A	3	1138	YYSSVRQRVTCEEPRFRECAAALIEGSATEVYAG EWRADRRSGFGVSQRSNGLRYEGEWLGNRRHG YGRTTRPDGSREEGKYKRNRLVHGGRVRSLLPL ALRRGKVKEKVDRAVEGARRAVSAARQRQEIA AARAADALLKAVAASSVAEKAVEAARMAKLIA QDLQPMLEAPGRRPRQDSEGSDTEPLDEDSPGV YENGLTPSEGSPELPSSPASSRQPWRPPACRSPLP PGGDQGPFSSPKAWPEEWGGAGAQAEELAGYE AEDEAGMQGPGPRDGSPLLGGCSDSSGSLREEE GEDEEPLPPLRAPAGTEPEPIAMLVLRGSSSRGPD AGCLTEELGEPAATERPAQPGAANPLVVGAVAL LDLSLAFLFSQLLT
3754	A	2	3338	SSLLEKMTSSDKDFRFMATSDLMSELQKDSIQLD

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				EDSERKVVKMLLRLLEDKNGEVQNLAVKWLGV PLGAFHASLLHCLLPQLSSPRLAVRKRAVGALGH LATACSTDLFVELADHLLDRLPGPRVPTSPTAIRT LIQCLGSVGRQAGHRLGAHLDRLVPLVEDFCNL DDDELRESCLQAFEAFLRKCPKEMGPHVPNVTS LCLQYIKHDPNYNYDSDEDEEQMETEDSEFSEQE SEDEYSDDDDMSWKVRRAAAKCIAALISSRPDL LPDFHCTLAPVLIRRFKEREENVKADVFTAYIVL LRQTRPPKGWLEAMEEPTQTGSNLHMLRGQVPL VVKALQRQLKDRSVRARQGCFSLLTELAGVLPG SLAEHMPVLVSGIIFSLADRSSSSTIRMDALAFLQ GLLGTEPAEAFHPHLPILLPPVMACVADSFYKIA AEALVVLQELVRALWPLHRPRMLDPEPYVGEMS AVTLARLRATDLDQEVKERAISCMGHLVGHLGD RLGDDLEPTLLLLLDRLRNEITRLPAIKALTLVAV SPLQLDLQPILAEALHILASFLRKNQRALRLATLA ALDALAQSQGLSLPPSAVQAVLAELPALVNESD MHVAQLAVDFLATVTQAQPASLVEVSGPVLSEL LRLLRSPLLPAGVLAAAEGFLQALVGTRPPCVDY AKLISLLTAPVYEQAVDGGPGLHKQVFHSLARC VAALSAACPQ\EAESTASRLVCDARSPHSSTGVK VLAFLSLAEVGQVAGPGHERELKAVLLEALGSPS EDVRAAASYALGRVGAGSLPDFLPFLLEQIEAEP RRQYLLLHSLKEALGAAQPDSLKPYAEDIWALL FQRCEGAEEGTRGVVAECIGKLVLVNPSFLLPRL RKQLAAGRPHTRSTVITAVKFLISDQPHPIDPLLK SFIAVHNKPSLVRDLLDDILPLLYQETKIRRDLIRE VEMGPFKHTVDDGLDVRKAAFECMYSLLESCLG QLDICEFLNHVEDGLKDHYDIRMLTFIMVARLAT LCPAPVLQRVDRLIEPLRATCTAKVKAGSVKQEF EKQDELKRSAMRAVAALLTIPEVGKSPIMADFSS QIRSNPELAALFESIQKDSTSAPSTDSMELS
3755	A	2	3338	SSLLEKMTSSDKDFRFMATSDLMSELQKDSIQLD EDSERKVVKMLLRLLEDKNGEVQNLAVKWLGV PLGAFHASLLHCLLPQLSSPRLAVRKRAVGALGH LATACSTDLFVELADHLLDRLPGPRVPTSPTAIRT LIQCLGSVGRQAGHRLGAHLDRLVPLVEDFCNL DDDELRESCLQAFEAFLRKCPKEMGPHVPNVTS LCLQYIKHDPNYNYDSDEDEEQMETEDSEFSEQE SEDEYSDDDDMSWKVRRAAAKCIAALISSRPDL LPDFHCTLAPVLIRRFKEREENVKADVFTAYIVL LRQTRPPKGWLEAMEEPTQTGSNLHMLRGQVPL VVKALQRQLKDRSVRARQGCFSLLTELAGVLPG SLAEHMPVLVSGIIFSLADRSSSSTIRMDALAFLQ GLLGTEPAEAFHPHLPILLPPVMACVADSFYKIA AEALVVLQELVRALWPLHRPRMLDPEPYVGEMS AVTLARLRATDLDQEVKERAISCMGHLVGHLGD RLGDDLEPTLLLLLDRLRNEITRLPAIKALTLVAV SPLQLDLQPILAEALHILASFLRKNQRALRLATLA ALDALAQSQGLSLPPSAVQAVLAELPALVNESD MHVAQLAVDFLATVTQAQPASLVEVSGPVLSEL LRLLRSPLLPAGVLAAAEGFLQALVGTRPPCVDY AKLISLLTAPVYEQAVDGGPGLHKQVFHSLARC VAALSAACPQ\EAESTASRLVCDARSPHSSTGVK VLAFLSLAEVGQVAGPGHERELKAVLLEALGSPS

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				EDVRAAASYALGRVGAGSLPDFLPFLLEQIEAEP RRQYLLLHSLKEALGAAQPDSLKPYAEDIWALL FQRCEGAEEGTRGVVAECIGKLVLVNPSFLLPRL RKQLAAGRPHTRSTVITAVKFLISDQPHPIDPLLK SFIAVHNKPSLVRDLLDDILPLLYQETKIRRDLIRE VEMGPFKHTVDDGLDVRKAAFECMYSLLESCLG QLDICEFLNHVEDGLKDHYDIRMLTFIMVARLAT LCPAPVLQRVDRLIEPLRATCTAKVKAGSVKQEF EKQDELKRSAMRAVAALLTIPEVGKSPIMADFSS QIRSNPELAALFESIQKDSTSAPSTDSMELS
3756	A	112	1361	SLEEQQGRHPSFAPKCASQILGRIMITLITEQLQK QTLDELKCTRFSISLPLPDHADISNCGNSFQLVSE GASWRGLPHCSCAEFQ/DQPQLQLPSLRPEPAPQ TT\HRGNSPKEQPFSQVLRPEPPDPEKLPVPPAPPS KRHCRSLSVPVDLSRWQPVWRPAPSKLWTPIKH RGSGGGGGPQVPHQSPPKRVSSL/SVPPSSQCLFS MCPSSHTLQPSFLQPGPGP\DSSRPCAASPQSGSW ESDAESLSPCPPQRRFSLSPSLGPQASRFLPSARSS PASSPELPWRPRGLRNLPRSRSQPCDLDARKTGV KRRHEEDPRRLRPSLDFDKMNQKPYSGGLCLQE TAREGSSISPPWFMACSPPPLSASCSPTGGSSQVL SESEEEEEGAVRWGRQALSKRTLCQRDFGDLDL NLIEEN
3757	A	413	1	PKPMLQQDFT/SLPDQGLDHIAE/NSYFDARSLCA AELVCKEWQQVTSE*MLWKKLIERMVHAYPLW KGLSEKVW/DQHLFKNRPTDGPPNSFHRSLYPKII QVIETIESNWQCG*HTLQRIQCHSEKSKGVYCLQ YDDEK
3758	A	2	613	FVSGSPWRMDGSTERLEARRPAGRLPWSSRQEM TRRPSLMAGRQHGWSAQQSATVANPVPGANPD LLPHFLGEPEDVYIVKNKPVLLVCKAVPATQIFF KCNGEWVRQVDHVIERSTDGSSGLPTMEVRINV SRQQVEKVFGLEEYWCQCVAWSSSGTTKSQKA YIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPEGI PPAE
3759	A	1	561	ADDTLHLWNLRQKRPAILHSLKFCRERVTFCHLP FQSKWLYVGTERGNIHIVNVESFTLSGYVIMWN KAIELSSKSHPGPVVHISDNPMDEGKLLIGFESGT VVLWDLKSKKADYRYTYDEAIHSVAWHHEGKQ FICSHSDGTLTIWNVRSPAKPVQTITPHGKQLKD GKKPEPCKPILKVEFXTTR
3760	A	1	824	LPACRCGCVAGCPSNHGICRCLRASERQVCVMH LKHLRTLLSPQDGAAKVTCMAWSQNNAKFAVC TVDRVVLLYDEHGERRDKFSTKPADMKYGRKS YMVKGMAFSPDSTKIAIGQTDNIIYVYKIGEDWG DKKVICNKFIQTVKFRPVPGTLG*TNIYQYIYL*IQ PGVAFLTSECDFSYCKDGASWLFMVICCLP*SPA VSFPIGD*\SAVTCLQWPAEYIIVFGLAEGKVRLS NTKTNKSSTIYGTESYVVSLTTNCSGKGILSGHA DGYQR
3761	A	2253	320	PVIQRCSQPYGFSLLISFFLKCVSETSQQPPSRKVF QLLPSFPTLTRSKSHESQLGNRIDDVSSMRFDLSH GSPQMVRRDIGLSVTHRFSTKSWLSQVCHVCQK SMIFGVKCKHCRLKCHNKCTKEAPACRISFLPLT RLRRTESVPSDINNPVDRAAEPHFGTLPKALTKK

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				EHPPAMNHLDSSSNPSSTTFSTPSSPAPFPTSSNPS SATTPP\NPSP\GQR\DSRFNFPSC/AYFIHHR\Q\QFI FPDISAFAHAAPLPEAADGTRLDDQPKADVLEAH EAEAEEPEAGKSEAEDDEDEVDDLPSSRRPWRG PISRKASQTSVYLQEWDIPFEQVELGEPIGQGRW GRVHRGRWHGEVAIRLLEMDGHNQDHLKLFKK EVMNYRQTRHENVVLFMGACMNPPHLAIITSFC KGRTLHSFVRDPKTSLDINKTRQIAQEIIKGMGYL HAKGIVHKDLKSRNVFYDNG\KVVITDFGLF\GIS GVVP\EGRRENQLKLSHDWLCYLAPEIVREMTPG KDEDQLPFSKAADVYAFGTVWYELQARDWPLK NQAAEASIWQIGSGEGMKRVLTSVSLGKEVSEN LSACWAFDLQERPS\FSLLMDMLEKLPKLNRRLS HPGHF*KSADINSSKVVPRFERFGLGVLESSNPK M
3762	A	2	1578	MAHYITFLCMVLVLLLQNSVLAEDGEVRSSCRT APTDLVFILDGSYSVGPENFEIVKKWLVNITKNF DIGPKFIQVGVVQYSDYPVLEIPLGSYDSGEHLTA AVESILYLGGNTKTGKAIQFALDYLFAKSSRFLT KIAVVLTDGKSQDDVKDAAQAARDSKITLFAIG VGSETEDAELRAIANKPSSTYVFYVEDYIAISKIR EVMKQKLCEESVCPTRIPVAARDERGFDILLGLD VNKKVKKRIQLSPKKIKGYEVTSKVDLSELTSNV FPEGLPPSYVFVSTQRFKVKKIWDLWRILTIDG/* PQIAVTLNGVDKILLFTTTSVINGSQVVTFANPQV KTLFDEGWHQIRLLVTEQDVTLYIDDQQIENKPL HPVLGILINGQTQIGKYSGKEETVQFDVQKLRIY CDPEQNNRETACEIPGFCLNGPSDVGSTPAPCICP PGKPGLQGPKGDPGLPGNPGYPGQPGQDGKPVS TESLVISGISGITGYQGIAGTPGVPGSPGIQGARGL PGYKGEPGRDGDK
3763	A	3	1267	CKVWRNPLNLFRGAEYNRYTWVTGREPLTYYD MNLSAQDHQTFFTCDSDHLRPADAIMQKAWRE RNPQARISAAHEALEINECATAYILLAEEEATTIA EAEKLFKQALKAGDGCYRRSQQLQHHGSQYEA QHSVLYLPLQ\TRHQCLGVHQKKASNVCQKTRE DQGSSENDERFNEGVPPSEYVQYP*KPF\KALLEL QAYADVQAVLAKYDDISLPKSATICYTAALLKA RAVSDKFSPEAASRRGLSTAEMNAVEAIHRAVEF NPHVPKYLLEMKSLILPPEHILKRGDSEAIAYAFF HLAHWKRVEGALNLLHCTWEGTFRMIPYPLEKG HLFYPYPICTETADRELLPSFHEVSVYPKKELPFFI LFTAGLCSFTAMLALLTHQFPELMGVFAKAVSV CLEGGLGEWMGKAKGIKAA
3764	A	25	1032	RSADGLCGNKDRERGNEFTRNQQAAQEVVNPK KKMKKKKYVNSGTVTLLSFAVESECTFLDYIKG GTQINFTVAIDFTASNGNPSQSTSLHYMSPYQLN AYALALTAVGEIIQHYDSDKMFPALGFGAKLPPD GRVSHEFPLNGNQENPSCCGIDGILEAYHRSLRT VQLYGPTNFAPVVTHVARNAAAVQDGSQYSVL LIITDGVISDMAQTKEAIVNG\SKLPMSIIIVGVGQ AEFNAMVELDGDDVRISSRGKLAERDIVQFVPFR DYVDRTGNHVLSMARLARDVLAEIPDQLVSYM KAQGIRPRSPPAAPTHSPSQSPARTPPACPLHTHI
3765	A	172	3456	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLG

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				KNFDSAKVPSDEYCPACKEKGKLKALKTYRISFQ ESIFLCEDLQCIYPLGSKSLNNLISPDLEECHTPHK PQKRKSLESSYKDSLLLANSKKTRNYIAIDGGKV LNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLE RNEILEADTVDMATTKDPATVDVSGTGRPSPQN EGCTSKLEMPLESKCTSFPQALCVQWKNAYALC WLDCILSALVHSEELKNTVTGLCSKEESIFWRLL TKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEI ETCLNEVRDEIFISLQPQLRCTLGDMESPVFAFPL LLKLETHIEKLFLYSFSWDFECSQCGHQYQNRH MKSLVTFTNVIPEWHPLNAAHFGPCNNCNSKSQI RKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHFE GCLYQITSVIQYRANNHFITWILDADGSWLECDD LKGPCSERHKKFEVPASEIHIVIWERKISQVTDKE AACLPLKKTNDQHALSNEKPVSLTSCSVGDAAS AETASVTHPKDISVAPRTLSQDTAVTHGDHLLSG PKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LEN KPVAENTGILKTNTLLSQESLMASSVSAPCNEKLI QDQFVDISFPSQVVNTNMQSVQLNTEDTVNTKS VNNTDATGLIQGVKSVEIEKDAQLKQFLTPKTEQ LKPERVTSQVSNLKKKETTADSQTTTSKSLQNQS LKENQKKPFVGSWVKGLISRGASFMPLCVSAHN RNTITDLQPSVKGVNNFGGFKTKGINQKASHVSK KARKSASKPPPISKPPAGPPSSNGTAAHPHAHAA SEVLEKSGSTSCGAQLNHSSYGNGISSANHEDLV EGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRT VRSENLEQVPQDGSPNDCESIEDLLNELPYPIDIA NESACTTVPGVSLYSSQTHEEILAELLSPTPVSTE LSENGEGDFRYLGMGDSHIPPPVPSEFNDVSQNT HLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTL NLESPMKTDIFDEFFSSSALNALANDTLDLPHFDE YLFENY
3766	A	3	1622	AQQIVYRNVMLENYKNLVSLGYQLTKPDVILRL EKGEEPWLVEREIHQETHPDSETAFEIKSSVSSRSI FKDKQSCDIKMEGMARNDLWYLSLEEVWKCRD QLDKYQENPERHLRQVAFTQKKVLTQERVSESG KYGGNCLLPAQLVLREYFHKRDSHTKSLKHDLV LNGHQDSCASNSNECGQTFCQNIHLIQFARTHTG DKSYKCPDNDNSLTHGSSLGISKGIHREKPYECK ECGKFFSWRSNLTRHQLIHTGEKPYECKECGKSF SRSSHLIGHQKTHTGEEPYECKECGKSFSWFSHL VTHQRTHTGDKLYTCNQCGKSF/VHSSRLIRHQR THTGEKPYECPECGKSFRQSTHLILHQRTHVRVR PYECNECGKSYSQRSHLVVHHRIHTGLKPFECKD CGKCFSRSSHLYSHQRTHTGEKPYECHDCGKSFS QSSALIVHQRIHTGEKPYECCQCGKAFIRKNDLIK HQRIHVGEETYKCNQCGIIFSQNSPFIVHQIAHTG EQFLTCNQCGTALVNTSNLIGYQTNHIRENAY
3767	A	3	1622	AQQIVYRNVMLENYKNLVSLGYQLTKPDVILRL EKGEEPWLVEREIHQETHPDSETAFEIKSSVSSRSI FKDKQSCDIKMEGMARNDLWYLSLEEVWKCRD QLDKYQENPERHLRQVAFTQKKVLTQERVSESG KYGGNCLLPAQLVLREYFHKRDSHTKSLKHDLV LNGHQDSCASNSNECGQTFCQNIHLIQFARTHTG DKSYKCPDNDNSLTHGSSLGISKGIHREKPYECK

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				ECGKFFSWRSNLTRHQLIHTGEKPYECKECGKSF SRSSHLIGHQKTHTGEEPYECKECGKSFSWFSHL VTHQRTHTGDKLYTCNQCGKSF/VHSSRLIRHQR THTGEKPYECPECGKSFRQSTHLILHQRTHVRVR PYECNECGKSYSQRSHLVVHHRIHTGLKPFECKD CGKCFSRSSHLYSHQRTHTGEKPYECHDCGKSFS QSSALIVHQRIHTGEKPYECCQCGKAFIRKNDLIK HQRIHVGEETYKCNQCGIIFSQNSPFIVHQIAHTG EQFLTCNQCGTALVNTSNLIGYQTNHIRENAY
3768	A	185	2258	SIIIKMSRKISKESKKVNISSSLESEDISLETTVPTD DISSSEEREGKVRITRQLIERKELLHNIQLLKIELS QKTMMIDNLKVDYLTKIEELEEKLNDALHQKQL LTLRLDNQLAFQQKDASKYQELMKQEMETILLR QKQLEETNLQLREKAGDVRRSLRDFELTEEQYIK LKAFPEDQLSIPEYVSVRFYELVNPLRKEICELQV KKNILAEELSTNKNQLKQLTETYEEDRKNYSEV QIRCQRLALELADTKQLIQQGDYRQENYDKVKS ERDALEQEVIELRRKHEILEASHMIQTKERSELSK EVVTLEQTVTLLQKDKEYLNRQNMELSVRCAHE EDRLERLQAQLEESKKAREEMYEKYVASRDHY KTEYENKLHDELEQIRLKTNQEIDQLRNASREMY ERENRNLREARDNAVAEKERAVMAEKDALEKH DQLLDRYRE\LQ\LSTESKVTEFLHQSKLKSFESE RVQLLQEETARNLTQCQLECEKYQKKLEVLTKE FYSLQASSEKRITELQAQNSEHQARLDIYEKLEK ELDEIIMQTAEIENEDEAERVLFSYGYGANVPTT AKRRLKQSVHLARRVLQLEKQNSLI/LKRSGTSK GPSNTAFTRSLTEANSLLNQTQQPYRYLIESVRQ RDSKIDSLTESIAQL/ERKDVSNLNKEKSALLQTN GIKMAL\DL\DQLLNHP
3769	A	3	2297	DAAEFRVVADAMKVIGFKPEEIQTVYKILAAILH LGNLKFVVDGDTPLIENGKVVSIIAELLSTKTDM VEKALLYRTVATGRDIIDKQHTEQEASYGRDAF AKAIYERLFCWIVTRINDIIEVKNYDTTIHGKNTV IGVLDIYGFEIFDNNSFEQFCINYCNEKLQQLFIQL VLKQEQEEYQREGIPWKHIDYFNNQIIVDLVEQQ HKGIIAILDDACMNVGKVTDEMFLEALNSKLGK HAHFSSRKLCASDKILEFDRDFRIRHYAGDVVYS VIGFIDKNKDTLFQDFKRLMYNSSNPVLKNMWP EGKLSITEVTKRPLTAATLFKNSMIALVDNLASK EPYYVRCIKPNDKKSPQIFDDERCRHQVEYLGLL ENVRVRRAGFAFRQTYEKFLHRYKMISEFTWPN HDLPSDKEAVKKLIERCGFQDDVAYGKTKIFIRT PRTLFTLEELRAQMLIRIVLFLQKVWRGTLARMR YKRTKAALTIIRYYRRYKVKSYIHEVARRFHGVK TMRDYGKHVKWPSPPKVLRRFEEALQTIFNRWR ASQLIKSIPASDLPQVRAKVAAVEMLKGQRADL GLQRAWEGNYLASKPDTPQTSGTFVPVANELKR KDKYMNVLFSCHVRKVNRFSKVEDRAIFVTDRH LYKMDPTKQYKVMKTIPLYNLTGLSVSNGKDQL VVFHTKDNKDLIVCLFSKQPTHESRIGEL\VGVLV NHFKSEKRHLQV\NVTNPVQCSLHGKKCTVSVE TRLNQPQPDFTKNRSGFILSVPGN
3770	A	3	6276	HKVAAPDVVVPTLDTVRHEALLYTWLAEHKPL VLCGPPGSGKTMTLFSALRALPDMEVVGLNFSS

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				ATTPELLLKTFDHYCEYRRTPNGVVLAPVQLGK WLVLFCDEINLPDMDKYGTQRVISFIRQMVEHG GFYRTSDQTWVKLERIQFVGACNPPTDPGRKPLS HRFLRHVPVVYVDYPGPASLTQIYGTFNRAMLR LIPSLRTYAEPLTAAMVEFYTMSQERFTQDTQPH YIYSPREMTRWVRGIFEALRPLETLPVEGLIRIWA HEALRLFQDRLVEDEERRWTDENIDTVALKHFP NIDREKAMSRPILYSNWLSKDYIPVDQEELRDYV KARLKVFYEEELDVPLVLFNEVLDHVLRIDRIFR QPQGHLLLIGVSGAGKTTLSRFVAWMNGLSVYQ IKVHRKYTGEDFDEDLRTVLRRSGCKNEKIAFIM DESNVLDSGFLERMNTLLANGEVPGLFEGDEYA TLMTQCKEGAQKEGLMLDSHEELYKWFTSQVIR NLHVVFTMNPSSEGLKDRAATSPALFNRCVLNW FGDWSTEALYQVGKEFTSKMDLEKPNYIVPDYM PVVYDKLPQPPSHREAIVNSCVFVHQTLHQANA RLAKRGGRTMAITPRHYLDFINHYANLFHEKRSE LEEQQMHLNVGLRKIKETVDQVEELRRDLRIKS QELEVKNAAANDKLKKMVKDQQEAEKKKVMS QEIQEQLHKQQEVIADKQMSVKEDLDKVEPAVI EAQNAVKSIKKQHLVEVRSMANPPAAVKLALES ICLLLGESTTDWKQIRSIIMRENFIPTIVNFSAEEIS DAIREKMKKNYMSNPSYNYEIVNRASLACGPMV KWAIAQLNYADMLKRVEPLRNELQKLEDDAKD NQQKANEVEQMIRDLEASIARYKEEYAVLISEAQ AIKADLAAVEAKVNRSTALLKSLSAERERWEKT SETFKNQMSTIAGDCLLSAAFIAYAGYFDQQMR QNLFTTWSHHLQQANIQFRTDIARTEYLSNADER LRWQASSLPADDLCTENAIMLKRFNRYPLIIDPS GQATEFIMNEYKDRKITRTSFLDDAFRKNLESAL RFGNPLLVQDVESYDPVLNPVLNREVRRTGGRV LITLGDQDIDLSPSFVIFLSTRDPTVEFPPDLCSRV TFVNFTVTRSSLQSQCLNEVLKAERPDVDEKRSD LLKLQGEFQLRLRQLEKSLLQALNEVKGRILDDD TIITTLENLKREAAEVTRKVEETDIVMQEVETVS QQYLPLSTACSSIYFTMESLKQIHFLYQYSLQFFL DIYHNVLYENPNLKGVTDHTQRLSIITKDLFQVA FNRVARGMLHQDHITFAMLLARIKLKGTVGEPT YDAEFQHFLRGNEIVLSAGSTPRIQGLTVEQAEA VVRLSCLPAFKDLIAKVQADEQFGIWLDSSSPEQ TVPYLWSEETPATPIGQAIHRLLLIQAFRPDRLLA MAHMFVSTNLGESFMSIMEQPLDLTQIVGTEVKP NTPVLMCSVPGYDASGHVEDLAAEQNTQITSIAI GSAEGFNQADKAINTAVKSGRWVMLKNVHLAP GWLMQLEKKLHSLQPHACFRLFLTMEINPKVPV NLLRAGRIFVFEPPPGVKANMLRTFSSIPVSRICK SPNERARLYFLLAWFHAIIQERLRYAPLGWSKKY EFGESDLRSACDTVDTWLDDTAKGRQNISPDKIP WSALKTLMAQSIYGGRVDNEFDQRLLNTFLERL FTTRSFDSEFKLACKVDGHKDIQMPDGIRREEFV QWVELLPDTQTPSWLGLPNNAERVLLTTQGVD MISKMLKMQMLEDEDDLAYAETEKKTRTDSTS DGRP\AWMRTLHTTASNWLHLIPQTLSHLKRTVE NIKDPLFRFFE\REVKMGAKLLQ\DVRQDLADV\V QVCEGKKKQTNYLRTLI\NELV\KGILP\RSWSHY

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				TVPAG\MTVIQWGVPISARRI\KQLQNISL\AAASG GAKELKNIHVCLGGGLFVPEAYITATRQYVAQAN SWSLEELCLEVNVTTSQGATLDACSFGVTGLKL QGATCNNNKLSLSNAISTALPLTQLRWVKQTNT EKKASVVTLPVYLNFTRADLIFTVDFEIATKEDPR SFYERGVAVLCTE
3771	A	1	2043	LPLLHAGFNRRFMENSSIIACYNELIQIEHGEVRS QFKLRACNSVFTALDHCHEAIEITSDDHVIQYVN PAFERMMGYHKGELLGKELADLPKSDKNRADL LDTINTCIKKGKEWQGVYYARRKSGDSIQQHVKI TPVIGQGGKIRHFVSLKKLCCTTDNNKQIHKIHR DSGDNSQTEPHSFRYKNRRKESIDVKSISSRGSDA PSLQNRRYPSMARIHSMTIEAPITKVINIINAAQEN SPVTVAEALDRVLEILRTTELYSPQLGTKDEDPH TSDLVGGLMTDGLRRLSGNEYVFTKNVHQSHSH LAMPITINDVPPCISQLLDNEESWDFNIFELEAITH KRPLVYLGLKVFSRFGVCEFLNCSETTLRAWFQ VIEANYHSSNAYHNSTHAADVLHATAFFLGKER VKGSLDQLDEVAALIAATVHDVDHPGRTNSFL\C NAGSELAVLYNDT\AV\LESHHTALAFQ\LTVKDT K\CNIFKNID/RGNHYRTLRQAIIDMVLATEMTKH FEHVNKFVNSINKPMAAEIEGSDCECNPAGKNFP ENQILIKRMMIKCADVANPCRPLDLCIEWAGRIS EEYFAQTDEEKRQGLPVVMPVFDRNTCSIPKSQI SFIDYFITDMFDAWDAFAHLPALMQHLADNYKH WKTLDDLKCKSLRLPSDRLKPSHRGGLLTDKGH CESQ
3772	A	1013	50	TLVHADGFPSLHITETCLAYREKRIGIDLVHDTVE HELIKEAEIIQGIMALLTRTLEEASEQIRMNRSAK YNLEKDLKDKFVALTIDDICFSLNNNSPNIRYSEN AVRIEPNSVSLEDWLDFSSTNVEKADKQRNNSL MLKALVD\RILSQTANYLRKQCDVVHTAFKNGL KDTKDARDQLADHLAK\VMEEIASQEKNITALEK AILDQEGPAKVAHTRLETRTHRPNVELCRDVAQ YRLMKEVQEITHNVARLKETLA\QAQAELKGLH RRQLALQEEIQVKENTIYIDEVLCMQMRKSIPLR DGEDHGVWAGGLRPDAVC
3773	A	1	955	AAARESERQLRLRLCVLNEILGTERDYVGTLRFL QSAFLHRIRQNVADSVEKGLTEENVKVLFSNIEDI LEVHKDFLAALEYCLHPEPQSQHELGNVFLKFK DKFCVYEEYCSNHEKALRLLVELNKIPTVRAFLL SCMLLGGRKTTDIPLEGYL\LSPIQRICKYPLLLKE LAKRTPGKHPDHPAVQ\SALQAMKTVCSNINETK RQMEKLEALEAAA/QSHIEGWEGSNLTDICTQLL LQGTLLKISAGNIQERAFFLFDNLLVYCKRKSRV TGSKKSTKRTKSINGSLYIFRGRINTEVMEVENVE DGTGSPSPSLA
3774	A	4254	2061	ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLI RVDGKGSIKELFPTGKQLEPLVAPLADGKVAVG QDDLTV.VLNEEGICTQKCALNWTDIPVAMEHQP PYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFITSGG SNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFE LALQLAEMKDDSDSEKQQQIHHIKNLYAFNLFC QKRFDESMQVFAKLGTDPTHVMGLYPDLLPTDY RKQLQYPNPLPVLSGAELEKAHLALIDYLTQKRS

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				QLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQII DTTLLKCYLHTNVALVAPLLRLENNHCHIEESEH VLKKAHKYSELIILYEKKGLHEKALQVLVDQSK KANSPLKGHERTVQYLQHLGTENLHLIFSYSVW VLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKV QGLMKEYLLSFPAGKTPVPAGEEEGELGEYRQK LLMFLEISSYYDPGRLICDFPFDGLLEERALLLGR MGKHEQALFIYVHILKDTRMAEEYCHKHYDRN KDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPK ANLQAALQVLELHHSKLDTTKALNLLPANTQIN DIRIFLEKVLEENAQKKRFNQVLKNLLHAEFLRV\ QEERILHQQVKCIITEEKVCMVCKKKIGNSAFAR YPNGVVVHYFCS\KEVNPADT
3775	A	1832	839	MSRARGALCRACLALAAALAALLLLPLPLPRAP APARTPAPAPRAPPSRPAAPSLRPDDVFIAVKTTR KNHGPRLRLLLRTW\ISRARQQTFIFTDGDDPELE LQGGDRVINTNCSAVRTRQALCCKMSVEYDKFI ESGRKWFCHVDDDNYVNARSLLHLLSSFSPSQD VYLGRPSLDHPIEATERVQGGRTVTTVKFWFAT GGAGFCLSRGLALKMSPWASLGSFMSTAEQVRL PDDCTVGYIVEGLLGARLLHSPLFHSHLENLQRL PPDTLLQQVTLSHGGPENPQNVVVNVAGGFSLHQ DPTRFKSIHCLLYPDTDWCPRQKQGAPTSR
3776	A	3	796	PRAKLGTRARNMAGQDAGCGRGGDDYSEDEGD SSVSRAAVEVFGKLKDLNCPFLEGLYITEPKTIQE LLCSPSEYRLEILEWMCTRVWPSLQDRFSSLKGV PTEVKIQEMTKLGHELMLCAPDDQELLKGCACA QKQLHFMDQLLDTIRSLTIGCSSCSSLMEHFEDT REKNEALLGELFSSPHLQMLLNPECDPWPLDMQ PLLNKQSDDWQWASASAKSEEEEKLAELARQLQ ESAAKLHALRTEYFAQHEQGAAAGAA\TSAP
3777	A	3	413	SEEDVIEGKTAVIEKRRKKRSSAGVVED/IGGEVQ NMLEGVGVDINKALLAKRKRLEMYTKASLRTSN QKIEHVWKTQQDQRQKLNQEYSQQFLTLFQQW DLDMQKAEEQEEKILVGIMIRFIINQVSSRNGQPS LLL
3778	A	132	788	SRLPPPPHLADGRAGARVPRSARLSRWWVQD WTHGPIVRPPAAARTMWVNPEEVLLANALWITE RANPYFILQRRKGHAGDGGGGGGLAGLLVGTLD VVLDSSARVAPYRILYQTPDSLVYWTIACG\GSR KEITEHWEWLEQNLLQTLSIFENENDITTFVRGKI QGIIAEYNKINDVKEDDDTEKFKEAIVKFHRLFG MPEEEKLVNYYSCSYWKG
3779	A	2	934	CKSCTLFPQNPNLPPPSTRERPPGCKTVFVGGLPE NATEEIIQEVFEQCGDITAIRKSKKNFCHIRFAEEF MVDKAIYLSGYRMRLGSSTDKKDSGRLHVDFA QARDDFYEWECKQRMRAREERHRRKLEEDRLR PPSPPAIMHYSEHEAALLAEKLKDDSKFSEAM\Q VLLSWIERGEVNRR\SANQFYSMVQSANSHVRRL MNEKATHEQEMEEAKENFKNALTGILTQFEQIV AVFNASTRQKAWDHFSKAQRKNIDIWAK\HSEE LRNAQSEQLMGIRREEEMEMSDDENCDSPTKKM RVDESALGAP
3780	A	1	2535	AAQAEREELAAGRMPGGGPQGAPAAAGGGGVS

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				HRAGSRDCLPPAACFRRRRLARRPGYMRSSTGP GIGFLSPAVGTLFRFPGGVSGEESHHSESRARQC GLDSRGLLVRSPVSKSAAAPTVTSVRGTSAHFGI QLRGGTRLPDRLSWPCGPGSAGWQQEFAAMDS SETLDASWEAACSDGARRVRAAGSLPSAELSSNS CSPGCGPEVPPTPPGSHSAFTSSFSFIRLSLGSAGE RGEAEGCPPSREAESHCQSPQEMGAKAASLDGP HEDPRCLSQPFSLLATRVSADLAQAARNSSRPER DMHSLPDMDPGSSSSLDPSLAGCGGDGSSGSGD AHSWDTLLRKWEPVLRDCLLRNRRQMEVISLRL KLQKLQEDAVENDDYDKAETLQQRLEDLEQEKI SLHFQLPSRQPALSSFLGHLAAQVQAALRRGATQ QASGDDTHTPLRMEPRLLEPTAQDSLHVSITRRD WLLQEKQQLQKEIEALQARMFVLEAKDQQLRRE IEEQEQQLQWQGCDLTPLVGQLSLGQLQEVSKA LQDTLASAGQIPFHAEPPETIRSLQERIKSLNLSLK EITTKVCMSEKFCSTLRKKVNDIETQLPALLEAK MHAISGNHFWTAKDLTEEIRSLTSDREGLEGLLS KLLVLSSRNVKKLGSVKEDYNRLRREVEHQETA YETSVKENTMKYMETLKNKLCSCKCPLLGKVW EADLEACRLLIQCLQLQEARGSLSVEDERQMDD LEGAAPPIPPRLHSEDKRKTPLKESYILSAELGEK CEDIGKKLLYLEDQLHTAIHSHDEDLIQSLRRELQ MVKETLQAMILQLQPAKEAGEREAAASCMTAG VHEAQA
3781	A	3	995	GRRRAGPAHSARMYNMMETELKPPGPQQTSGG GGGNSTAAAAGGNQKNSPDRVKRPMNAFMVW SRGQRRKMAQENPKMHNSEISKRLGAEWKLLSE TEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTK TLMKKDKYTLPGGLLAPGGNSMASGVGVGAGL GAGVNQRMDSYAHMNGWSNGSYSMMQDQLG YPQHPGLNAHGAAQMQPMHRYDVSALQYNSM TSSQTYMNG/SRPTYSMSYSQQGTPGMAPGS\MG SVVKSEASSSPPVVTSSSHSRAPCQAGDLRDMIS MYLPGAEVPEPAAPSRLHMSQHYQSGPVPGTAI NGTLPLSHM
3782	A	1	2649	FRVPDSCPVVLHSFTQLDPDLPRPESSTQEIGEELI NGVIYSISLRKVQLHHGGNKGQRWLGYENESAL NLYETCKVRTVKAGTLEKLVEHLVPAFQGSDLS YVTIFLCTYRAFTTTQQVLDLLFKRYGRCDALTA SSRYGCILPYSDEDGGPQDQLKNAISSILGTWLD QYSEDFCQPPDFPCLKQLVAYVQLNMPGSDLER RAHLLLAQLEHSEPIEAEPEGEEDWALSPVPALK PTPELELALTPARAPSPVPAPAPEPEPAPTPAPGSE LEVAPAPAPELQQAPEPAVGLESAPAPALELEPA PEQDPAPSQTLELEPAPAPVPSLQPSWPSPVVAEN GLSEEKPHLLVFPPDLVAEQFTLMDAELFKKVVP YHCLGSIWSQRDKKGKEHLAPTIRATVTQFNSV ANCVITTCLGNRSTKAPDRARVVEHWIEVAREC RILKNFSSLYAILSALQSNSIHRLKKTWEDVSRDS FRIFQKLSEIFSDENNYSLSRELLIKEGTSKFATLE MNPKRAQKRPKETGIIQGTVPYLGTFLTDLVML DTAMKDYLYGRLINFEKRRKEFEVIAQIKLLQSA CNNYSIAPDEQFGAWFRAVERLSETESYNLSCEL EPPSESASNTLRTKKNTAIVKRWSDRQAPSTELS

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				TSGSSHSKSCDQLRCGPYLSSGDIADALSVHSAG SSSSDVEEINISFVPESPDGQEKKFWESASQSSPET SGISSASSSTSSSSASTTPVAATRTHKRSVSGLCNS SSALPLYNQQVGDCCIIRVSLDVDNGNMYKSILV TSQDKAPAVIRKAMDKHNLEEEEPEDYELLQILS DDRKLKIPENANVFYAMNSTANYDFVLKKRTFT KGVKVKHGASSTLPRMKQKGLKIAKGIF
3783	A	3	869	RSGQGKVYGLIGRRRFQQMDVLEGLNLLITISGK RNKLRVYYLSWLRNKILHNDPEVEKKQGWTTV GDMEGCGHYRVVKYERIKFLVIALKSSVEVYAW APKPYHKFMAFKSFADLPHRPLLVDLTVEEGQR LKVIYGSSAGFHAVDVDSGNSYDIYIPVHIQSQIT PHAIIFLPNTDGMEMLLCYEDEGVYVNTYGRIIK DVVLQWGEMPTSVAYICSNQIMGWGEKAIEIRS VETGHLDGVFMHKRAQRLKFLCERNDKVFFASV RSGGSSQVYFMTLNRNCIMNW
3784	A	1213	457	LSPRQVDGLAGLQKGLSLSLLYQFLMNGIRLGTY GLAEAGGYLHTAEGTHSPARSAAAGAMAGVMG AYLGSPIYMVKTHLQAQAASEIAVGHQYKHQG MFQALTEIGQKHGLVGLWRGALGGLPRVIVGSS TQLCTFSSTKDLLSQWEIFPPQSWKLALVAAMM SGIAVVLAMAPFDVACTRLYNQPHRCTGQGP\LY RGILDALLQTARTEGIFGMYKGIGASYFRLGPHTI LSLFFWDQLRSLYYTDTK
3785	A	193	813	RRRGRHSLCGGKMLAYCVQDATVVDVEKRRNP SKHYVYIINVTWSDSTSQTIYRRY\SKFFDLQMQL LD\KFPI\ESGQKDPKQRIIPFLPGKILFRRSHIRDV AVKRLKPIDEYCRALVRLPPHISQCDEVFRFFEAR PEDVNPPKEQGPSPPDAVLPYGVNKGKQELKAG PNWPGRTHHVVNCVTQKCLFVFHFKFSSSGNKE SKSL
3786	A	3785	1632	EFVGRAASTTVVTRIAWRMADAGIRRVVPSDLY PLVLGFLRDNQLSEVANKFAKATGATQQDANAS SLLDIYSFWLNRSAKVPERKLQANGPVAKKAKK KASSSDSEDSSEEEEEVQGPPAKKAAVPAKRVGL PPGKAAAKASESSSSEESSDDDDEEDQKKQPVQ KGVKPQAKAGQAPPKKAKSSDSDSDSSSEDEPP KNQKPKITP\VTVKAQTKAPPKPARA\APKIANGK AASSSSSSSSSSSSSSDDSEEEKAAATPKKTVPKKQV VAKAPVKAATTPTRKSSSSEDSSSDEEEEQKKPM KNKPGPYSSVPPPSAPPPKKSLGTQPPKKAVEKQ QPVESSEDSSDESDSSSEEEKKPPTKAVVSKATTK PPPAKKAAESSSDSSDSDSSEDDEAPSKPAGTTK NSSNKPAVTTKSPAVKPAAAPKQPVGGGQKLLT RKADSSSSEEESSSSEEEKTKKMVATTKPKATAK AALSLPAKQAPQGSRDSSSDSDSSSSEEEEEKTSK SAVKKKPQKVAGGAAPSKPASAKKGKAESSNSS SSDDSSEEEEEKLKGKGSPRPQAPKANGTSALTA QNGKAAKNSEEEEEEKKKAAVVVSKSGSLKKR KQNEAAKEAETPQAKKIKLQTPNTFPKRKKGEK RASSPFRRVREEEIEVDSRVADNSFDAKRGAAGD WGERANQVLKFTKGKSFRHEKTKKKRGSYRGG SISVQVNSIKFDSE
3787	A	3	5078	IPEG/RALSAEHTSSLVPSLHITTLGQEQAILSGAV PASPSTGTADFPSILTFLQPTENHASPSPVPEMPTL

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				PAEGSDGSPPATRDLLLSSKVPNLLSTSWTFPRW KKDSVTAILGKNEEANVTIPLQAFPRKEVLSLHT VNGFVSDFSTGSVSSPIITAPRTNPLPSGPPLPSILS IQATQTVFPSLLAFSSTKPEVYAAAVDHSGLPAS APKQVRASPSSMDVYDSLTIGDMKKPATTDVFW SSLSAETGSLSTESIISGLQQQTNYDLNGHTISTTS WETHLAPTAPPNGLTSAADAIKSQDFKDTAGHS VTAEGFSIQDLVLGTSIEQPVQQSDMTMVGSHID LWPTSNNNHSRDFQTAEVAYYSPTTRHSVSHPQ LQLPNQPAHPLLLTSPGPTSTGSLQEMLSDGTDT GSEISSDINSSPERNASTPFQNILGYHSAAESSISTS VFPRTSSRVLRASQHPKKWTADTVSSKVQPTAA AAVTLFLRKSSPPALSAALVAKGTSSSPLAVASG PAKSSSMTTLAKNVTNKAASGPKRTPGAVHTAF PFTPTYMYARTGHTTSTHTA/IARKHGHCLWPVV YNLP/PP/GKPQAMHTGLPNPTNLEMPRASTPRPL TVTAALTSITASVKATRLPPLRAENTDAVLPAAS AAVVTTGKMASNLECQMSSKLLVKTVLFLTQRR VQISESLKFSIAKGLTQALRKAFHQNDVSAHVDI LEYSHNVTVGYYATKGKLVYLPAVVIEMLGVY GVSNVTADLKQHTPHLQSVAVLASPWNPQPAG YFQLKTVLQFVSQADNIQSCKFAQTMEQRLQKA FQDAERKVLNTKSNLTIQIVSTSNASQAVTLVYV VGNQSTFLNGTVASSLLSQLSAELVGFYLTYPPL TIAEPLEYPNLDISETTRDYWVITVLQGVDNSLV GLHNQSFARVMEQRLAQLFMMSQQQGRRFKRA TTLGSYTVQMVKMQRVPGPKDPAELTYYTLYN GKPLLGTAAAKILSTIDSQRMALTLHHVVLLQAD PVVKNPPNNLWIIAAVLAPIAVVTVIIIIITAVLCR KNKNDFKPDTMINLPQRAKPVQGFDYAKQHLG QQGADEEVIPVTQETVVLPLPIRDAPQERDVAQD GSTIKTAKSTETRKSRSPSENGSVISNESGKPSSGR RSPQNVMAQQKVTKEEARKRNVPASDEEEGAV LFDNSSKVAAEPFDTSSGSVQLIAIKPTALPMVPP TSDRSQESSAVLNGEVNKALKQKSDIEHYRNKL RLKAKRKGYYDFPAVETSKGLTERKKMYEKAP KEMEHVLDPDSELCAPFTESKNRQQMKNSVYRS RQSLNSPSPGETEMDLLVTRERPRRGIRNSGYDT EPEIIEETNIDRVPEPRGYSRSRQVKGHSETSTLSS QPSIDEVRQQMHMLLEEAFSLASAGHAGQSRHQ EAYGSAQHLPYSEVVTSAPGTMTRPRAGVQWVP TYRPEMYQYSLPRPAYRFSQLPEMVMGSPPPPVP PRTGPVAVASLRRSTSDIGSKTRMAESTGPEPAQ LHDSASFTQMSRGPVSVTQLDQSALNYSGNTVP AVFAIPAANRPGFTGYFIPTPPSSYRNQAWMSYA GENELPSQWADSVPLPGYIEAYPRSRYPQSSPSRL PRQYSQPANLHPSLEQAPAPSTAASQQSLAENDP SDAPLTNISTAALVKAIREEVAKLAKKQTDMFEF QV
3788	A	2	1737	MKGLYTDAEMKSDNVKDKDAKISFLQKAIDVV VMVSGEPLLAKPARIVAGHEPERTNELLQIIGKC CLNKLSSDDAVRRVLAGEKGEVKGRASLTSRSQ ELDNKNVREEESRVHKNTEDRGDAEIKERSTSRD RKQKEELKEDRMPREKDKDKEKAKENGGNRHR EGERERAKARARPDNERQKDRGNRERDRDSERK

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				KETERKSEGGKEKERLRDRDRERDRDKGKDRDR RRVKNGEHSWDLDRENNREHDKPEKKSASSGE MSKKLSDGTFKDSKAETETEISTRASKSLTTKTS KRRSKNSVEGDSTSDAEGDAGPAGQDKSEVPET PEIPNELSSNIRRIPRPGSARPAPPRVKRQDSMEAL QMDRSGSGKTVSNVITESHNSDNEEDDQFVVEA APQLSEMSEIEMVTAVELEEEEKHGGLVKKILET KKDYEKLQQSPKPGEKERSLFESAWKKEKDIVS KEIEKLRTSIQTLCKSALPLGKIMDYIQEDVDAM QNELQM\YHSENRQHAEALQQEQRITDCAVEP\L KAELA\ELEQLIKD\Q\QDKICAVKANILKNEEKIQ KMVYSINLTSRR
3789	A	1	4369	MRTLGTCLATLAGLLLLTAAGETFSGGCLFDEPYS TCGYSQSEGDDFNWEQVNTLTKPTSDPWMPSGS FMLVNASGRPEGQRAHLLLPQLKENDTHCIDFH YFVSSKSNSPPGLLNVYVKVNNGPLGNPIWNISG DPTRTWNRAELAISTFWPNFYQVIFEVITSGHQG YLAIDEVKVLGHPCTRTPHFLRIQNVEVNAGQFA TFQCSAIGRTVAGDRLWLQGIDVRDAPLKEIKVT SSRRFIASFNVVNTTKRDAGKYRCMI\RTEGGVGI SNYAEL\VVKEPPVPIAPPQLASVGATYLWIQLN ANSINGDGPIVAREVEYCTASGSWNDRQPVDSTS YKIGHLDPDTEYEISVLLTRPGEGGTGSPGPALRT RTKCADPMRGPRKLEVVEVKSRQITIRWEPFGY NVTRCHSYNLTVHYCYQVGGQEQVREEVSWDT ENSHPQHTITNLSPYTNVSVKLILMNPEGRKESQ ELIVQTDEDLPGAVPTESIQGSTFEEKIFLQWREP TQTYGVITLYEITYKAVSSFDPEIDLSNQSGRVSK LGNETHFLFFGLYPGTTYSFTIRASTAKGFGPPAT NQFTTKISAPSMPAYELETPLNQTDNTVTVMLKP AHSRGAPVSVYQIVVEEERPRRTKKTTEILKCYP VPIHFQNASLLNSQYYFAAEFPADSLQAAQPFTIG DNKTYNGYWNTPLLPYKSYRIYFQAASRANGET KIDCVQVATKGAATPKPVPEPEKQTDHTVKIAG VIAGILLFVIIFLGVVLVMKKRKL\AKKRKETMSS TRQEIDLWIGELNGPRSYAEQGTKLATRAFSFMD THNLNGRSVSSPSSFTMKTNTLSTSVPNSYYPDE THTMASDTSSLVQSHTYKKREPADVPYQTGQLH PAIRVADLLQHITQMKCAEGYGFKEEYESFFEGQ SAPWDSAKKDENRMKNRYGNIIAYDHSRVRLQT IEGDTNSDYINGNYIDGYHRPNHYIATQGPMQET IYDFWRMVWHENTASIIMVTNLVEVGRVKCCK YWPDDTEIYKDIKVTLIETELLAEYVIRTFAVEKR GVHEIREIRQFHFTGWPDHGVPYHATGLLGFVR QVKSKSPPSAGPLVVHCSAGAGRTGCFIVIDIML DMAEREGVVDIYNCVRELRSRRVNMVQTEEQY VFIHDAILEACLCGDTSVPASQVRSLYYDMNKLD PQTNSSQIKEEFRTLNMVTPTLRVEDCSIALLPRN HEKNRCMDILPPDRCLPFLITIDGESSNYINAALM DSYKQPSAFIVTQHPLPNTVKDFWRLVLDYHCTS VVMLNDVDPAQLCPQYWPENGVHRHGPIQVEF VSADLEEDIISRIFRIYNAARPQDGYRMVQQFQFL GWPMYRDTPVSKRSFLKLIRQVDKWQEEYNGG EGRTVVHCLNGGGRSGTFCAISIVCEMLRHQRTV DVFHAVKTLRNNKPNMVDLLDQYKFCYEVALE

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				YLNSG
3790	A	261	485	EEQTPLHIASRLGKTEIVQLLLQHMAHPDAATTN GYTPLHISAREGQV\DV\ASVLLGRQGAAHSFRLT KVRRMTS
3791	A	1	5874	LPPVTMSGKYIMEEHDSYSDQVWSIDELPSKQG YYLQGNYLRCVAEVGSFEHNLTTDLLNHLVFVQ KVFMKEVNEVIQKVSGGEQPIPLWNEHDGTADG DKPKILLYSLNLQFKGIQVTATTPSMRAVRFETG LIELELSNRLQTKASPGSSSYLKLFGKCQVDLNL ALGQIVKHQVYEEAGSDFHQVAYFKTRIGLRNA LREEISGSSDREAVLITLNRPIVYAQPVAFDRAVL FWLNYK\AAYDNWNEQRMALHKDIHMATKEVV DMLPGIQQTSAQAFGTPFLQLTVNDLGICLPITNT AQSNHTGDLDTGSALVLTIESTLITACSSESLVSK GHFKNFCIRFADGFETSWDDWKPEIHGDLVMNA CVVPDGTYEVCSRTTGQAAAESSSAGTWTLNVL WKMCGIDVHMDPNIGKRLNALGNTLTTLTGEED IDDIADLNSVNIADLSDEDEVDTMSPTIHTEATDY RRQAASASQPGELRGRKIMKRIVDIRELNEQAKV IDDLKKLGASEGTINQEIQRYQQLESVAVNDIRR DVRKKLRRSSMRAASLKDKWGLSYKPSYSRSKS ISASGRPPLKRMERASSRVGETEELPEIRVDAASP GPRVTFNIQDTFPEETELDLLSVTIEGPSHYSSNSE GSCSVFSSPKTPGGFSPGIPFQTEEGRRDDSLSSTS EDSEKDEKDEDHERERFYIYRKPSHTSRKKATGF AAVHQLFTERWPTTPVNRSLSGTATERNIDFELD IRVEIDSGKCVLHPTTLLQEHDDISLRRSYDRSSR SLDQDSPSKKKKFQTNYASTTHLMTGKKVPSSL QTKPSDLETTVFYIPGVDVKLHYNSKTLKTESPN ASRGSSLPRTLSKESKLYGMKDSATSPPSPPLPST VQSKTNTLLPPQPPPIPAAKGKGSGGVKTAKLYA WVALQSLPEEMVISPCLLDFLEKALETIPITPVER NYTAVSSQDEDMGHFEIPDPMEES\TTSLVS\SSTS AYSSFPVDVVVYVRVQPSQIKFSCLPVSRVECML KLPSLDLVFSSNRGELETLGTTYPAETLSPGGNA TQSGTKTSASKTGIPGSSGLGSPLGRSRHSSSQSD LTSSSSSSSGLSFTACMSDFSLYVFHPYGAGKQIT AVSGLTPGSGGLGNVDEEPTSVTGRKDSLSINLE FVKVSLSRIRRSGGASFFESQSVSKSASKMDTTLI NISAVCDIGSASFKYDMRRLSEILAFPRAWYRRSI ARRLFLGDQTINLPTSGPGTPDSIEGVSQHLSPESS RKAYCKTWEQPSQSASFTHMPQSPNVFNEHMTN STMSPGTVGQSLKSPASIRSRSVSDSSVPRRDSLS KTSTPFNKSNKAASQQGTPWETLVVFAINLKQL NVQMNMSNVMGNTTWTTSGLKSQGRLSVGSNR DREISMSVGLGRSQLDSKGGVVGGTIDVNALEM VAHISEHPNQQPSHKIQITMGSTEARVDYMGSSIL MGIFSNADLKLQDEWKVNLYNTLDSSITDKSEIF VHGDLKWDIFQVMISRSTTPDLIKIGMKLQEFFT QQFDTSKRALSTWGPVPYLPPKTMTSNLEKSSQE QLLDAAHHRHWPGVLKVVSGCHISLFQIPLPEDG MQFGGSMSLHGNHMTLACFHGPNFRSKSWALF HLEEPNIAFWTEAQKIWEDGSSDHSTYIVQTLDF HLGHNTMVTKPCGALESPMATITKITRRRHENPP HGVASVKEWFNYVTATRNEELNLLRNVDANNT

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				ENSTTVKNSSLLSGFRGGSSYNHETETIFALPRM QLDFKSIHVQEPQEPSLQDASLKPKVECSVVTEF TDHICVTMDAELIMFLHDLVSAYLKEKEKAIFPP RILSTRPGQKSPIIIHDDNSSDKDREDSITYTTVDW RDFMCNTWHLEPTLRLISWTGRKIDPVGVDYILQ KLGFHHARTTIPKWLQRGVMDPLDKVLSVLIKK LGTALQDEKEKKGKDKEEH
3792	A	1	364	QNGSTPLHHAASKNRHEIALMLLEGGANPDGKD HYEATAKHQATAKGNFKMIHILLYYKASTIIQDT EGNTPPHLVCD\RVEEAKLLVSQGA/SIYIENKEE KDP/LQVAKGALGLVLKRMVEG
3793	A	2	340	DIVPNPKMAPLGDEAPTLEKVLTPELSEEEVSTR DDIQFHHFSSEEALQKVKYFVAKEDPSSQEEAHT PEAPPPQPPSSERCLGEMKCTLVRGDSSPRQAEL KSGPASRPAL
3794	A	421	158	SYWVGEDYTYKFFEVILIDPFHKAIRRNPDTQWI SKAVYKHREMCGLTSTGRKSHGLEKDRMFPHAI GGSCRAA*RRRKTLQFPCYH
3795	A	24	592	GGMDSRVSGTTSNGETKPVYPVMEKKEEDGTLE RGHWNNKMEFVLSVAGEIIGLGNVWRFPYLCYK NGGGAFFIPYLVFLFTCGIPVFLLETALGQYTSQG GVTAWRKICPIFEGIGYASQMIVILLNVYYIIVLA WALFYLFSSFTIDLPWGGCYHEWNTEHCMEFQK TNGSLNGTSENATSPVIEFW
3796	A	3	592	KPASTYSTSQPSMAPLLPIRTLPLILILLALLSPGA ADFNISSLSGLLSPALTESLLVALPPCHLTGGNAT LMVRRANDSKVVTSSFVVPPCRGRRELVSVVDS GAGFTVTRLSAYQVTNLVPGTKFYISYLVKKGT ATESSREIPMFTLPRRNMESIGLGMARTGGMVVI TVLLSVAMFLLVLGFIIALALGSRK
3797	A	1	1556	ATRLLRGSGSWGCSRLRFGPPAYRRFSSGGAYPN IPLSSPLPGVPKPVFATVDGQEKFETKVTTLDNGL RVASQNKFGQFCTVGILINSGSRYEAKYLSGIAH FLEKLAFSSTARFDSKDEILLTLEKHGGICDCQTS RDTTMYAVSADSKGLDTVVALLADVVLQPRLT DEEVEMTRMAVQFELEDLNLRPDPEPLLTEMIHE AAYRENTVGLHRFCPTENVAKINREVLHSYLRN YYTPDRMVLAGVGVEHEHLVDCARKYLLGVQP AWGSAEAVDIDRSVAQYTGGIAKLERDMSNVSL GPTPIPELTHIMVGLESCSFLEEDFIPFAVLNMMM GGGGSFSAGGPGKGMFSRLYLNVLNRHHWMYN ATSYHHSYEDTGLLCIHASADPRQVREMVEIITK EFILMGGTVDTVELERAKTQLTSMLMMNLESRP VIFEDVGRQVLATRSRKLPHELCTLIRNVKPEDV KRVASKMLRGKPAVAALGDLTDLPTYEHIQTAL SSKDGRLPRTYRLFR
3798	A	73	759	KRLVEAGVPRTFDGIVGEGGAQSRSCWPWGVTA QTPAFSADSLNCLKNCMSITMGSVRPSVEQFHKY LPWFLNDRPNIKCPKGGLAAYSTSVNLTSDGQV LASRFMAYHKPLKNSQDYTEALRAARELAANIT ADLRKVPGTDPAFEVFPYTITNVFYEQYLTILPEG LFMLSLCLVPTFAVSCLLLGLDLRSGLLNLLSIV MILVDTVGFMALWGISYNAVSLINLVS
3799	A	73	759	KRLVEAGVPRTFDGIVGEGGAQSRSCWPWGVTA QTPAFSADSLNCLKNCMSITMGSVRPSVEQFHKY

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				LPWFLNDRPNIKCPKGGLAAYSTSVNLTSDGQV LASRFMAYHKPLKNSQDYTEALRAARELAANIT ADLRKVPGTDPAFEVFPYTITNVFYEQYLTILPEG LFMLSLCLVPTFAVSCLLLGLDLRSGLLNLLSIV MILVDTVGFMALWGISYNAVSLINLVS
3800	A	250	1032	GIFRSLRVLFPLFSVGRPQFARSLSAAPQLSDTAD TMGFGDLKSPAGLQVLNDYLADKSYIEGYVPSQ ADVAVFEAVSSPPPADLCHALRWYNHIKSYEKE KASLPGVKKALGKYGPADVEDTTGSGATDSKD DDDIDLFGSDDEEESEEAKRLREERLAQYESKKA KKPALVAKSSILLDVKPWDDETDMAKLEECVRS IQADGLVWGSSKLVPVGYIKKLQIQCVVEDDK VGTDMLEEQITAFEDYVQSMDVAAFNKI
3801	A	155	656	SREMELVTFRDVAIEFSPEEWKCLDPAQQNLYR DVMLENYRNLVSLGFVISNPDLVTCLEQIKEPCN LKIHETAAKPPAICSPFSQDLSPVQGIEDSFHKLIL KRYEKCGHENLQLRKGCKRVNECKVQKGVNNG VYQCLSTTQSKIFQCNTCVRVFSTSSHSNKHK
3802	A	1	1428	VTVSPETHMDLTKGCVTFEDIAIYFSQDEWGLLD EAQRLLYLEVMLENFALVASLGCGHGTEDEETP SDQNVSVGVSQSKAGSSTQKTQSCEMCVPVLKD ILHLADLPGQKPYLVGECTNHHQHQKHHSAKKS LKRDMDRASYVKCCLFCMSLKPFRKWEVGKDL PAMLRLLRSLVFPGGKKPGTITECGEDIRSQKSH YKSGECGKASRHKHTPVYHPRVYTGKKLYECSK CGKAFRGKYSLVQHQRVHTGERPWECNECGKF FSQTSHLNDHRRIHTGERPYECSECGKLFRQNSS LVDHQKIHTGARPYECSQCGKSFSQKATLVKHQ RVHTGERPYKCGECGNSFSQSAILNQHRRIHTGA KPYECGQCGKSFSQKATLIKHQRVHTGERPYKC GDCGKSFSQSSILIQHRRIHTGARPYECGQCGKSF SQKSGLIQHQVVHTGERPYECNKCGNSFSQCSSL IHHQKCHNT
3803	A	193	617	LFPFLGSESKNGEADSSDKEMKHGQKSPTGKQTS QHLKRLKKSGLGHLKWTKAEDIDIETPGSILVNT NLRALINKHTFASLPQHFQQYLLLLLPEVDRQMG SDGILRLSTSALNNEFFAYAAQGWKQRLAEGKF VFSIIM
3804	A	197	479	SSSRASPPEHPSSQAHCGPLVLSHACPEVTNKWS TGSSSSPNSSWVSSPLQPEGLSGSSRMKGGSATKI LLETLLLAAHMTADQGIASSQRCLL
3805	A	1	385	QSADTLFPGDINFNVSGLFSAVTLQDTVSDRLAS EELPSTAVPTPATTPAPAPAPAPATAPALVSAAT KERTESEVPPRPASPKVTRSPPETAAPVEDMARR SELAVGGEEGTEGGRGEGTGSPMSSY
3806	A	47	1033	LQGDTWHLSFLSHFSRLHGGVPGRGLLEGNLLQ PQAPGHDMTSIPFPGDRLLQVDGVILCGLTHKQA VQCLKGPGQVARLVLERRVPRSTQQCPSANDSM GDERTAVSLVTALPGRPSSCVSVTDGPKF*SSN* KRIANGLGFSFVQMEKESCSHLKSDLVRIKRLFP GHPAEENGAIAAGDIILGREWEGPRKASSSRCRG SWAMQLSVQAGPSFASYYPAAVEVLHLLRGAPQ EVTLLLCRPPPGALPELEQEWQTPELSADKEFTR ATCTDSCTSPILGSRGQLGGTVPPQMQGKAWGL RPESSQKAIREGTMGAKTERDLGPVP

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3807	A	656	1238	RCPSLLPPSWPLPTLQTLTRTPGNKAIAGGAGLW AVLWGSERTPPYR*GN*NQRGAVPCLRPHRLRP QDKFLVLASDGLWDMLSNEDVVRLVVGHLAEA DWHKTDLAQRPANLGLMQSLLLQRKASGLHEA DQNAATRLIRHAIGNNEYGEMEAERLAAMLTLP EDLARMYRDDITVTVVYFNSESIGAYYKGG
3808	A	26	2195	SQYSESVAGRQASPERLLGSYHAMASTVEGGDT ALLPEFPRGPLDAYRARASFSWKELALFTEGEG MLRFKKTIFSALENDPLFARSPGADLSLEKYREL NFLRCKRIFEYDFLSVEDMFKSPLKVPALIQCLG MYDSSLAAKYLLHSLVFGSAVYSSGSERHLTYIQ KIFRMEIFGCFALTELSHGSNTKAIRTTAHYDPAT EEFIIHSPDFEAAKFWVGNMGKTATHAVVFAKL CVPGDQCHGLHPFIVQIRDPKTLLPMPGVMVGDI GKKLGQNGLDNGFAMFHKVRVPRQSLLNRMGD VTPEGTYVSPFKDVRQRFGASLGSLSSGRVSIVSL AILNLKLAVAIALRFSATRRQFGPTEEEEIPVLEY PMQQWRLLPYLAAVYALDHFSKSLFLDLVELQR GLASGDRSARQAELGREIHALASASKPLASWTT QQGIQECREACGGHGYLAMNRLGVLRDDNDPN CTYEGDNNILLQQTSNYLLGLLAHQVHDGACFR SPLKSVDFLDAYPGILDQKFEVSSVADCLDSAVA LAAYKWLVCYLLRETYQKLNQEKRSGSSDFEAR NKCQVSHGRPLALAFVELTVVQRFHEHVHQPSV PPSLRAVLGRLSALYALWSLSRHAALLYRGGYF SGEQAGEVLESAVLALCSQLKDDAVALVDVIAP PDFVLDSPIGRADGELYKNLWGAVLQESKVLER ASWWPEFSVNKPVIGSLKSKL
3809	A	117	830	CFGIMERVGCTLTTTYAHPRPTPTNFLPAISTMAS SYRDRFPHSNLTHSLSLPWRPSTYYKVASNSPSV APYCTRSQRVSENTMLPFVSNRTTFFTRYTPDDW YRSNLTNYQESNTSRHNSEKLRVDTSRLIQDKYQ QTRKTQADTTQNLGERVNDIGFWKSEIIHELDEM IGETNALTDVKKRLERALMETEAPLQVARECLF HREKRMGIDLVHDEVEAQLLTVNVGEMHQSQA A
3810	A	3	518	VIQELEGGSGADLGEHSCRPASQPRFPRPAEARS HPATRRPASGPAMGKTNSKLAPEVLEDLVQNTE FSEQELKQWYKGFLKDCPSGILNLEEFQQLYIKF FPYGDASKFAQHAFRTFDKNGDGTIDFREFICAL SVTSRGSFEQKLNWAFEMYDLDGDGRITRLEML EIIE
3811	A	81	1147	GCGYGCSGAGGAAIGEPMAKWGEGDPRWIVEE RADATNVNNWHWTERDASNWSTDKLKTLFLAV QVQNEEGKCEVTEVSKLDGEASINNRKGKLIFFY EWSVKLNWTGTSKSGVQYKGHVEIPNLSDENSV DEVEISVSLAKDEPDTNLVALMKEEGVKLLREA MGIYISTLKTEFTQGMILPTMNGESVDPVGQPAL KTEERKAKPAPSKTQARPVGVKIPTCKITLKETFL TSPEELYRVFTTQELVQAFTHAPATLEADRGGKF HMVDGNVSGEFTDLVPEKHIVMKWRFKSWPEG HFATITLTFIDKNGETELCMEGRGIPAPEEERTRQ GWQRYYFEGIKQTFGYGARLF
3812	A	20	558	PCGTAASTHAYDRRAKCRQQQQQQQNGGQNKV RPAKKKTSPAREVSSESGTSGQFTPPSSTSVPTIAS

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				SSAPVSIWSPASISPLSDPLSTSSSCMQRSYPMTYT QASGYSQGYAGSTSYFGGMDCGSYLTPMHHQL PGPGATLSPMGTNAVTSHLNQSPASLSTQGYGAS KLWGFNFNH
3813	A	1	1016	CTEPPRRSTRTPAALASLRPYTDYVVVSDQILQES EDFFTLIESHEGKPLKLMVYNSKSDSCREVTVTP NAAWGGEGSLGCGIGYGYLHRIPTQPPSYHKKPP GTPPPSALPLGAPPPDALPPGPTPEDSPSLETGSRQ SDYMEALLQAPGSSMEDPLPGPGSPSHSAPDPDG LPHFMETPLQPPPPVQRVMDPGFLDVSGISLLDN SNASVWPSLPSSTELTTTAVSTSGPEDICSSSSSHE RGGEATWSGSEFEVSFLDSPGAQAQADHLPQLT LPDSLTSAASPEDGLSAELLEAQAEEEPASTEGLD TGTEAEGLDSQAQISTTE*HPGL*QGP
3814	A	2	884	VFWQVRNAGSSPLSAACPLFRTPAPQPCGSWGR CCIPHASTGCRPMAERGELDLTGAKQNTGVWLV KVPKYLSQQWAKASGRGEVGKLRIAKTQGRTE VSFTLNEDLANIHDIGGKPASVSAPREHPFVLQSV GGQTLTVFTESSSDKLSLEGIVVQRAECRPAASE NYMRLKRLQIEESSKPVRLSQQLDKVVTTNYKP VANHQYNIEYERKKKEDGKRARADKQHVLDML FSAFEKHQYYNLKDLVDITKQPVVYLKEILKEIG VQNVKGIHKNTWELKPEYRHYQGEEKSD
3815	A	17	411	NIGDWEDIGKSPERIIQYYGPATWAQDGSRGYCT PIYMLNHIIRLQAVLEIIMNERANALDLLAQQTTK MRNANYQNRLALDYLLAHEGGV*GKFSLTNCC LEIDDNGKAIMEITARMRKLAHIPVQTWER
3816	A	3	1172	SHWQRRDRRCVRNMAERGRKRPCGPGEHGQRI EWRKWKQQKKEEKKKWKDLKLMKKLERQRAQ EEQAKRLEEEEAAAEKEDRGRPYTLSVALPGSIL DNAQSPELRTYLAGQIARACAIFCVDEIVVFDEE GQDAKTVEGEFTGVGKKGQACVQLARILQYLEC PQYLRKAFFPKHQDLQFAGLLNPLDSPHHMRQD EESEFREGVVVDRPTRPGHGSFVNCGMKKEVKI DKNLEPGLRVTVRLNQQQHPDCKTYHGKVVSS QDPRTKAGLYWGYTVRLASCLSAVFAEAPFQDG YDLTIGTSERGSDVASAQLPNFRHALVVFGGLQG LEAGADADPNLEVAEPSVLFDLYVNTCPGQGSR TIRTEEAILISLAALQPGLIQAGARHT
3817	A	246	1197	FLSAGMSNFTHYAYLLMIESLMLGKVPPHVPSH HFIFHDDGSARQKGESDYKVIIQQWFSKSGPWTT SSNVTWGLLELQQSISESAVLTIPPGDSGAGSNLI TMFLRNRKETDLCSGRSKVNRGWNSGRCKQRG KTEQPGEPLEHVYVTIKHAVALESRHQKGELQC LIKMCIPLSKPLQMFFSPPHWEAWLQRVQQLAK NTRYFRQRLQEMGFIIYGNENASVVPLLLYMPG KVAAFARHMLEKKIGVVVVGFPATPLAEARARF CVSAAHTREMLDTVLEALDEMGDLLQLKYSRH KKSARPELYDETSFELED
3818	A	215	789	NPQSSSSEGSSEIFQVNGHNRLLVQRSEVTQAPG QYTVDVEGHGCTFIQATLKYNVLLPKKASGFSLS LEIVKNYSSTAFDLTVTLKYTGIRNKSSMVVIDV KMLSGFTPTMSSIEELENKGQVMKTEVKNDHVL FYLENVFGRADSFTFSVEQSNLVFNIQPAPGMVY DYYEKEEYALAFYHINSSSVSE

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3819	A	1	1483	RIPDSIISRGVQGLPRDTASLSTTPSESPRAQATSR LSTASCPTPKVQSRCSSKENILRASHSAVDITKVA RRHRMSPFPLTSMDKAFITVLEMTPVLGTEIINYR DGMGRVLAQDVYAKDNLPPFPASVKDGYAVRA ADGPGDRFIIGESQAGEQPTQTVMPGQVMRVTT GAPIPCGADAVVQVEDTELIRESDDGTEELEVRIL VQARPGQDIRPIGHDIKRGECVLAKGTHMGPSEI GLLATVGVTEVEVNKFPVVAVMSTGNELLNPED DLLPGKIRDSNRSTLLATIQEHGYPTINLGIVGDN PDDLLNALNEGISRADVIITSGGVSMGEKDYLKQ VLDIDLHAQIHFGRVFMKPGLPTTFATLDIDGVR KIIFALPGNPVSAVVTCNLFVVPALRKMQGILDP RPTIIKARLSCDVKLDPRPEYHRCILTWHHQEPLP WAQSTGNQMSSRLMSMRSANGLLMLPPKTEQY VELHKGEVVDVMVIGRL
3820	A	2216	487	PQEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCK QVCSTVGGSAICSCFPGYAIMADGVSCEDQDECL MGAHDCSRRQFCVNTLGSFYCVNHTVLCADGYI LNAHRKCVDINECVTDLHTCSRGEHCVNTLGSF HCYKALTCEPGYALKDGECEDVDECAMGTHTC QPGFLCQNTKGSFYCQARQRCMDGFLQDPEGNC VDINECTSLSEPCRPGFSCINTVGSYTCQRNPLIC ARGYHASDDGTKCVDVNECETGVHRCGEGQVC HNLPGSYRCDCKAGFQRDAFGRGCIDVNECWAS PGRLCQHTCENTLGSYRCSCASGFLLAADGKRC EDVNECEAQRCSQECANIYGSYQCYCRQGYQLA EDGHTCTDIDECAQGAGILCTFRCLNVPGSYQCA CPEQGYTMTANGRSCKDVDECALGTHNCSEAET CHNIQGSFRCLRFECPPNYVQVSKTKCERTTCHD FLECQNSPARITHYQLNFQTGLLVPAHIFRIGPAP AFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYL QRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHI FFTTFAL
3821	A	2216	487	PQEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCK QVCSTVGGSAICSCFPGYAIMADGVSCEDQDECL MGAHDCSRRQFCVNTLGSFYCVNHTVLCADGYI LNAHRKCVDINECVTDLHTCSRGEHCVNTLGSF HCYKALTCEPGYALKDGECEDVDECAMGTHTC QPGFLCQNTKGSFYCQARQRCMDGFLQDPEGNC VDINECTSLSEPCRPGFSCINTVGSYTCQRNPLIC ARGYHASDDGTKCVDVNECETGVHRCGEGQVC HNLPGSYRCDCKAGFQRDAFGRGCIDVNECWAS PGRLCQHTCENTLGSYRCSCASGFLLAADGKRC EDVNECEAQRCSQECANIYGSYQCYCRQGYQLA EDGHTCTDIDECAQGAGILCTFRCLNVPGSYQCA CPEQGYTMTANGRSCKDVDECALGTHNCSEAET CHNIQGSFRCLRFECPPNYVQVSKTKCERTTCHD FLECQNSPARITHYQLNFQTGLLVPAHIFRIGPAP AFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYL QRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHI FFTTFAL
3822	A	2502	1540	MAAATRGCRPWGSLLGLLGLVSAAAAAWDLAS LRCTLGAFCECDFRPDLPGLECDLAQHLAGQHL AKALVVKALKAFVRDPAPTKPLVLSLHGWTGTG KSYVSSLLAHYLFQGGLRSPRVHHFSPVLHFPHP

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				SHIERYKKDLKSWVQGNLTACGRSLFLFDEMDK MPPGLMEVLRPFLGSSWVVYGTNYRKAIFIFISN TGGEQINQVALEAWRSRRDREEILLQELEPVISR AVLDNPHHGFSNSGIMEERLLDAVVPFLPLQRHH VRHCVLNELAQLGLEPRDEVVQAVLDSTTFFPE DEQLFSSNGCKTVASRIAFFL
3823	A	1	3174	YGCEKTTEGRIPLKNIYRLFSADRKRVETALEAC SLPSSRNDSIPQEDFTPEVYRVFLNNLCPRPEIDNI FSEFGAKSKPYLTVDQMMDFINLKQRDPRLNEIL YPPLKQEQVQVLIEKYEPNNSLARKGQISVDGFM RYLSGEENGVVSPEKLDLNEDMSQPLSHYFINSS HNTYLTAGQLAGNSSVEMYRQVLLSGCRCVELD CWKGRTAEEEPVITHGFTMTTEISFKEVIEAIAEC AFKTSPFPILLSFENHVDSPKQQAKMAEYCRLIFG DALLMEPLEKYPLESGVPLPSPMDLMYKILVKN KKKSHKSSEGSGKKKLSEQASNTYSDSSSMFEPS SPGAGEADTESDDDDDDDDCKKSSMDEGTAGSE AMATEEMSNLVNYIQPVKFESFEISKKRNKSFEM SSFVETKGLEQLTKSPVEFVEYNKMQLSRIYPKG TRVDSSNYMPQLFWNAGCQMVALNFQTMDLA MQINMGMYEYNGKSGYRLKPEFMRRPDKHFDP FTEGIVDGIVANTLSVKIISGQFLSDKKVGTYVEV DMFGLPVDTRRKAFKTKTSQGNAVNPVWEEEPI VFKKVVLPTLACLRIAVYEEGGKFIGHRILPVQAI RPGYHYICLRNERNQPLTLPAVFVYIEVKDYVPD TYADVIEALSNPIRYVNLMEQRAKQLAALTLEDE EEVKKEADPGETPSEAPSEARTTPAENGVNHTTT LTPKPPSQALHSQPAPGSVKAPAKTEDLIQSVLTE VEAQTIEELKQQKSFVKLQKKHYKEMKDLVKR HHKKTTDLIKEHTTKYNEIQNDYLRRRAALEKS AKKDSKKKSEPSSPDHGSSTIEQDLAALDAEMTQ KLIDLKDKQQQQLLNLRQEQYYSEKYQKREHIK LLIQKLTDVAEECQNNQLKKLKEICEKEKKELKK KMDKKRQEKITEAKSKDKSQMEEEKTEMIRSYI QEVVQYIKRLEEAQSKRQEKLVEKHKEIRQQILD EKPKLQVELEQEYQDKFKRLPLEILEFVQEAMKG KISEDSNHGSAPLSLSSDPGKVNHKTPSSEELGGD IPGKEFDTPL
3824	A	1	426	ILHWFVHRWSGRNNREKIGVHVGFEEILNMEPY CCRETLKSLRPECFIYDLSAVVMHHGKGFGSGH YTAYCYNSEGGFWVHCNDSKLSMCTMDEVCKA QAYILFYTQRVTENGHSKLLPPELLLGSQHPNED ADTSSNEILS
3825	A	3	364	GIRAKFPNKIPVVVERYPRETFLPPLDKTKFLVPQ ELTMTQFLSIIRSRMVLRATEAFYLLVNNKSLVS MSATMAEIYRDYKDEDGFVYMTYASQETFGCLE SAAPRDGSSLEDRPLHPL
3826	A	1	1237	PEKKFERECREAEKAQQSYERLDNDTNATKADV EKAKQQLNLRTHMADENKNEYAAQLQNFNGEQ HKHFYVVIPQIYKQLQEMDERRTIKLSECYRGFA DSERKVIPIISKCLEGMILAAKSVDERRDSQMVV DSFKSGFEPPGDFPFEDYSQHIYRTISDGTISASKQ ESGKMDAKTTVGKAKGKLWLFGKKPKGPALED FSHLPPEQRRKKLQQRIDELNRELQKESDQKDAL NKMKDVYEKNPQMGDPGSLQPKLAETMNNIDR

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				LRMEIHKNEAWLSEVEGKTGGRGDRRHSSDINH LVTQGRESPEGSYTDDANQEVRGPPQQHGHHNE FDDEFEDDDPLPAIGHCKAIYPFDGHNEGTLAMK EGEVLYIIEEDKGDGWTRARRQNGEEGYVPTSYI DVTLEKNSKGS
3827	A	2	1584	INPVSSAVNGEAHSSHETRGQNSNALPSVLLELL SQSCLIPAMSSYLRNDSVLDMARHVPLYRALLEL LRAIASCAAMVPLLLPLSTENGEEEEEQSECQTS VGTLLAKMKTCVDTYTNRLRSKRENVKTGVKP DASDQEPEGLTLLVPDIQKTAEIVYAATTSLRQA NQEKKLGEYSKKAAMKPKPLSVLKSLEEKYVAV MKKLQFDTFEMVSEDEDGKLGFKVNYHYMSQV KNANDANSAARARRLAQEAVTLSTSLPLSSSSSV FVRCDEERLDIMKVLITGPADTPYANGCFEFDVY FPQDYPSSPPLVNLETTGGHSVRFNPNLYNDGKV CLSILNTWHGRPEEKWNPQTSSFLQVLVSVQSLI LVAEPYFNEPGYERSRGTPSGTQSSREYDGNIRQ ATVKWAMLEQIRNPSPCFKEVIHKHFYLKRVEIM AQCEEWIADIQQYSSDKRVGRTMSHHAAALKRH TAQLREELLKLPCPEGLDPDTDDAPEVCRATTGA EETLMHDQVKPSSSKELPSDFQL
3828	A	1415	845	PRVPATLVSLDPWHCFPTAGRLAGSTWVPPACT LQLGPSSEHELDNHRAPLLSLPSQESLSFTPWYLV ACKPLFHIFCPLFACFMQEGKVQYLFLHL'SHMRL LNYYFFPFLAPESLMQALEDLDYLAALDNDGNL SEFGIIMSEFPLDPQLSKSILASCEFDCVDEVLTIA AMVTGILNDYSFSFFANLH
3829	A	199	683	VDHTPVLSKPQCFSSVKWGATLSARSQKTSGIGR LMVHVIEATELKACKPNGKSNPYCEISMGSQSYT TRTIQDTLNPKWNFNCQFFIKDLYQDVLCLTLFD RDQFSPDDFLGRTEIPVAKIRTEQESKGPMTRRLL LHEVPTGEVWVRFDLQLFEQKTLL
3830	A	1747	404	RKMMEESGIETTPPGTPPPNPAGLAATAMSSTPV PLAATSSFSSPNVSSMESFPPLAYSTPQPPLPPVRP SAPLPFVPPPAVPSVPPLVTSMPPPVSPSTAAAFG NPPVSHFPPSTSAPNTLLPAPPSGPPISGFSVGSTY DITRGHAGRAPQTPLMPSFSAPSGTGLLPTPITQQ ASLTSLAQGTGTTSAITFPEEQEDPRITRGQDEAS AGGIWGFIKGVAGNPMVKSVLDKTKHSVESMIT TLDPGMAPYIKSGGELDIVVTSNKEVKVAAVRD AFQEVFGLAVVVGEAGQSNIAPQPVGYAAGLKG AQERIDSLRRTGVIHEKQTAVSVENFIAELLPDK WFDIGCLVVEDPVHGIHLETFTQATPVPLEFVQQ AQSLTPQDYNLRWSGLLVTVGEVLEKSLLNVSR TDWHMAFTGMSRRQMIYSAARAIAGMYKQRLP PRTV
3831	A	5	674	FWTRSAWHEGLQQMKANDPSLQEVNLYNIKNIP IPTLREFAKALETNTHVKKFSLAATRSNDPVAIAF ADMLKVNTTLTSLNIESHFITGTGILALVEALKEN DTLTEIKIDNQRQQLGTAVEMEIAQMLEENSRIL KFGYQFTKQGPRTRVAAAITKNNDLAWQKDTQ EQTSIWQVVSQSIAGFNPQFEVQGQNARSWMEE LGKAFHQFVRRELKQTEGKLP
3832	A	164	782	EPWVPMDVAESPERDPHSPEDEEQPQGLSDDDIL RDSGSDQDLDGAGVRASDLEDEESAARGPSQEE

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				EDNHSDEEDRASEPKSQDQDSEVNELSRGPTSSP CEEEGDEGEEDRTSDLRDEASSVTRELDEHELDY DEEVPEEPAPAVQEDEAEKAGAEDDEEKGEGTP REEGKAGVQSVGEKESLEAAKEKKKEDDDGEID DEEMY
3833	A	122	1676	SQPPHFTQKMNENKDTDSKKSEEYEDDFEKDLE WLINENEKSDASIIEMACEKEENINQDLKENETV MEHTKRHSDPDKSLQDEVSPRRNDIISVPGIQPLD PISDSDSENSFQESKLESQKDLEEEEDEEVRRYIM EKIVQANKLLQNQEPVNDKRERKLKFKDQLVDL EVPPLEDTTTSKNYFENERNMFGKLSQLCISNDF GQEDVLLSLTNGSCEENKDRTILVERDGKFELLN LQDIASQGFLPPINNANSTENDPQQLLPRSSNSSV SGTKKEDSTAKIHAVTHSSTGEPLAYIAQPPLNR KTCPSSAVNSDRSKGNGKSNHRTQSAHISPVTST YCLSPRQKELQKQLEEKREKLKREEERRKIEEEK EKKRENDIVFKAWLQKKREQVLEMRRIQRAKEI EDMNSRQENRDPQQAFRLWLKKKHEEQMKERQ TEELRKQEECLFFLKGTEGRERAFKQWLRRKRM EKMAEQQAVRERTRQLRLEAKRSKQLQHHLYM SEAKPFRFTDHYN
3834	A	575	774	RSRTEELSNSGILKAMSKDLVTFGDVAVNFSQEE WEWLNPAQRNLYRKVMLENYRSLVSLGKDMSP
3835	A	2	100	ASDFYLRYYVGHKGKFGHEFLEFEFRPDGVYV
3836	A	91	749	RPTPGHGDFWMQPLTKDAGMSLSSVTLASALQV RGEALSEEEIWSLLFLAAEQLLEDLRNDSSDYVV CPWSALLSAAGSLSFQGRVSHIEAAPFKAPELLQ GQSEDEQPDASQMHVYSLGMTLYWSAGFHVPP HQPLQLCEPLHSILLTMCEDQPHRRCTLQSVLEA CRVHEKEVSVYPAPAGLHIRRLVGLVLGTISEVS REPCFSSSSCWSCVAIKI
3837	A	3	1214	SLGCTNSARGKGQDDEVRTLMANGAPFTTDWFS KLRVSCGYIGDNCKNGADVNAKDMLKMTALH WATERHHRDVVELLIKYGADVHAFSKFDKSAFD IALEKNNAEILVILQEAMQNQVNVNPERANPVTD PVSMAAPFIFTSGEVVNLASLISSTNTKTTSGDPH ASTVQFSNSTTSVLATLAALAEASVPLSNSHRAT ANTEEIIEGNSVDSSIQQVMGSGGQRVITIVTDGV PLGNIQTSIPTGGIGHPFIVTVQDGQQVLTVPAGK VAEETVIKEEEEEKLPLTKKPRIGEKTNSVEESKE GNERELLQQQLQEANRRAQEYRHQLLKKEQEAE QYRLKLEAIARQQPNGVDFTMVEEVAEVDAVV VTEGELEERETKVTGSAGATGPPTRVSMATVSS
3838	A	1	1332	MIEDNKENKDHSLERGRASLIFSLKNEVGGLIKA LKIFQEKHVNLLHIESRKSKRRNSEFEIFVDCDIN REQLNDIFHLLKSHTNVLSVNLPDNFTLKEDGME TVPWFPKKISDLDHCANRVLMYGSELDADHPGF KDNVYRKRRKYFADLAMNYKHGDPIPKVEFTEE EIKTWGTVFQELNKLYPTHACREYLKNLPLLSKY CGYREDNIPQLEDVSNFLKERTGFSIRPVAGYLSP RDFLSGLAFRVFHCTQYVRHSSDPFYTPEPDTCH ELLGHVPLLAEPSFAQFSQEIGLASLGASEEAVQ KLATCYFFTVEFGLCKQDGQLRVFGAGLLSSISE LKHALSGHAKVKPFDPKITCKQECLITTFQDVYF VSESFEDAKEKMREFTKTIKRPFGVKYNPYTRSI

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				QILKDTKSITSAMNELQHDLDVVSDALAKVSRKP SI
3839	A	3093	520	MVNFTVDQIRAIMDKKANIRNMSVIAHVDHGKS TLTDSLVCKAGIIASARAGETRFTDTRKDEQERCI TIKSTAISLFYELSENDLNFIKQSKDGAGFLINLID SPGHVDFSSEVTAALRVTDGALVVVDCVSGVCV QTETVLRQAIAERIKPVLMMNKMDRALLELQLE PEELYQTFQRIVENVNVIISTYGEGESGPMGNIMI DPVLGTVGFGSGLHGWAFTLKQFAEMYVAKFA AKGEGQLGPAERAKKVEDMMKKLWGDRYFDP ANGKFSKSATSPEGKKLPRTFCQLILDPIFKVFDA IMNFKKEETAKLIEKLDIKLDSEDKDKEGKPLLK AVMRRWLPAGDALLQMITIHLPSPVTAQKYRCE LLYEGPPDDEAAMGIKSCDPKGPLMMYISKMVP TSDKGRFYAFGRVFSGLVSTGLKVRIMGPNYTPG KKEDLYLKPIQRTILMMGRYVEPIEDVPCGNIVG LVGVDQFLVKTGTITTFEHAHNMRVMKFSVSPV VRVAVEAKNPADLPKLVEGLKRLAKSDPMVQCI IEESGEHIIAGAGELHLEICLKDLEEDHACIPIKKS DPVVSYRETVSEESNVLCLSKSPNKHNRLYMKA RPFPDGLAEDIDKGEVSARQELKQRARYLAEKY EWDVAEARKIWCFGPDGTGPNILTDITKGVQYL NEIKDSVVAGFQWATKEGALCEENMRGVRFDV HDVTLHADAIHRGGGQIIPTARRCLYASVLTAQP RLMEPIYLVEIQCPEQVVGGIYGVLNRKRGHVFE ESQVAGTPMFVVKAYLPVNESFGFTADLRSNTG GQAFPQCVFDHWQILPGDPFDNSSRPSQVVAETR KRKGLKEGIPALDNFLDKL
3840	A	2	753	SSTRSRDFCCSEAIQGSLTRRERRASGVRTRRSQG SSAMASKILLNVQEEVTCPICLELLTEPLSLDCGH SLCRACITVSNKEAVTSMGGKSSCPVCGISYSFE HLQANQHLANIVERLKEVKLSPDNGKKRDLCDH HGEKLLLFCKEDRKVICWLCERSQEHRGHHTVL TEEVFKECQEKLQAVLKRLKKEEEEAEKLEADIR EEKTSWKYQVQTERQRIQTEFDQLRSILNNEEQR ELQRLEEEEKKT
3841	A	2	405	GKAFSCFTYLSQHRRTHMAEKPYECKTCKKAFS HFGNLKVHERIHTGEKPYECKECRKAFSWLTCL LRHERIHTGKKSYECQQCGKAFTRSRFLRGHEKT HTGEKMHECKECGKALSSLSSLHRHKRTHWRDT L
3842	A	311	88	AVLKNMAPMTALGLLDLHILNLILFLSAGEDFTS VVSEIMMYILLVFLTLWLLIEMIYCYRKVSKAEE AAQENA
3843	A	3	1175	APIRNSRIDDFVRRVESKATSARCGLWGSGPRRR PASGMFRGLSSWLGLQQPVAGGGQPNGDAPPEQ PSETVAESAEEELQQAGDQELLHQAKDFGNYLF NFASAATKKITESVAETAQTIKKSVEEGKIDGIID KTIIGDFQKEQKKFVEEQHTKKSEAAVPPWVDT NDEETIQQQILALSADKRNFLRDPPAGVQFNFDF DQMYPVALVMLQEDELLSKMRFALVPKLVKEE VFWRNYFYRVSLIKQSAQLTALAAQQQAAGKEE KSNGREQDLPLAEAVRPKTPPVVIKSQLKTQEDE EEISTSPGVSEFVSDAFDACNLNQEDLRKEMEQL VLDKKQEETAVLEEDSADWEKELQQELQEYEV

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				VTESEKRDENWDKEIEKMLQEEN
3844	A	798	148	LPPAQIPEAWLLLANVVVVLILVPLKDRLIDPLLL RCKLLPSALQKMALGMFFGFTSVIVAGVLEMER LHYIHHNETVSQQIGEVLYNAAPLSIWWQIPQYL LIGISEIFASIPGLEFAYSEAPRSMQGAIMGIFFCLS GVGSLLGSSLVALLSLPGGWLHCPKDFGNINNCR MDLYFFLLAGIQAVTALLFVWIAGRYERASQGP ASHSRFSRDRG
3845	A	3	1934	PEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWI MRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDS METIYNMLVETGELDNTYIVYTADHGYHIGQFG LVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIV LNIDLAPTILDIAGLDIPADMDGKSILKLLDTERP VNRFHLKKKMRVWRDSFLVERGKLLHKRDNDK VDAQEENFLPKYQRVKDLCQRAEYQTACEQLG QKWQCVEDATGKLKLHKCKGPMRLGGSRALSN LVPKYYGQGSEACTCDSGDYKLSLAGRRKKLFK KKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAA QPRNLTKRHWPGAPEDQDDKDGGDFSGTGGLP DYSAANPIKVTHRCYILENDTVQCDLDLYKSLQ AWKDHKLHIDHEIETLQNKIKNLREVRGHLKKK RPEECDCHKISYHTQHKGRLKHRGSSLHPFRKGL QEKDKVWLLREQKRKKKLRKLLKRLQNNDTCS MPGLTCFTHDNQHWQTAPFWTLGPFCACTSAN NNTYWCMRTINETHNFLFCEFATGFLEYFDLNT DPYQLMNAVNTLDRDVLNQLHVQLMELRSCKG YKQCNPRTRNMDLGLKDGGSYEQYRQFQRRKW PEMKRPSSKSLGQLWEGWEG
3846	A	3	1934	PEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWI MRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDS METIYNMLVETGELDNTYIVYTADHGYHIGQFG LVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIV LNIDLAPTILDIAGLDIPADMDGKSILKLLDTERP VNRFHLKKKMRVWRDSFLVERGKLLHKRDNDK VDAQEENFLPKYQRVKDLCQRAEYQTACEQLG QKWQCVEDATGKLKLHKCKGPMRLGGSRALSN LVPKYYGQGSEACTCDSGDYKLSLAGRRKKLFK KKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAA QPRNLTKRHWPGAPEDQDDKDGGDFSGTGGLP DYSAANPIKVTHRCYILENDTVQCDLDLYKSLQ AWKDHKLHIDHEIETLQNKIKNLREVRGHLKKK RPEECDCHKISYHTQHKGRLKHRGSSLHPFRKGL QEKDKVWLLREQKRKKKLRKLLKRLQNNDTCS MPGLTCFTHDNQHWQTAPFWTLGPFCACTSAN NNTYWCMRTINETHNFLFCEFATGFLEYFDLNT DPYQLMNAVNTLDRDVLNQLHVQLMELRSCKG YKQCNPRTRNMDLGLKDGGSYEQYRQFQRRKW PEMKRPSSKSLGQLWEGWEG
3847	A	1	1257	MVFSAVLTAFHTGTSNTTFVVYENTYMNITLPPP FQHPDLSPLLRYSFETMAPTGLSSLTVNSTAVPTT PAAFKSLNLPLQITLSAIMIFILFVSFLGNLVVCLM VYQKAAMRSAINILLASLAFADMLLAVLNMPFA LVTILTTRWIFGKFFCRVSAMFFWLFVIEGVAILL IISIDRFLIIVQRQDKLNPYRAKVLIAVSWATSFCV AFPLAVGNPDLQIPSRAPQCVFGYTTNPGYQAYV

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				ILISLISFFIPFLVILYSFMGILNTLRHNALRIHSYPE GICLSQASKLGLMGLQRPFQMSIDMGFKTRAFTT ILILFAVFIVCWAPFTTYSLVATFSKHFYYQHNFF EISTWLLWLCYLKSALNPLIYYWRIKKFHDACLD MMPKSFKFLPQLPGHTKRRIRPSAVYVCGEHRT VV
3848	A	3	2827	SSAVAARRRRSWASLVLAFLGVCLGITLAVDRS NFKTCEESSFCKRQRSIRPGLSPYRALLDSLQLGP DSLTVHLIHEVTKVLLVLELQGLQKNMTRFRIDE LEPRRPRYRVPDVLVADPPIARLSVSGRDENSVE LTMAEGPYKIILTARPFRLDLLEDRSLLLSVNARG LLEFEHQRAPRVSQGSKDPAEGDGAQPEETPRD GDKPEETQGKAEKDEPGAWEETFKTHSDSKPYG PMSVGLDFSLPGMEHVYGIPEHADNLRLKVTEG GEPYRLYNLDVFQYELYNPMALYGSVPVLLAHN PHRDLGIFWLNAAETWVDISSNTAGKTLFGKMM DYLQGSGETPQTDVRWMSETGIIDVFLLLGPSISD VFRQYASLTGTQALPPLFSLGYHQSRWNYRDEA DVLEVDQGFDDHNLPCDVIWLDIEHADGKRYFT WDPSRFPQPRTMLERLASKRRKLVAIVDPHIKVD SGYRVHEELRNLGLYVKTRDGSDYEGWCWPGS AGYPDFTNPTMRAWWANMFSYDNYEGSAPNLF VWNDMNEPSVFNGPEVTMLKDAQHYGGWEHR DVHNIYGLYVHMATADGLRQRSGGMERPFVLA RAFFAGSQRFGAVWTGDNTAEWDHLKISIPMCL SLGLVGLSFCGADVGGFFKNPEPELLVRWYQMG AYQPFFRAHAHLDTGRREPWLLPSQHNDIIRDAL GQRYSLLPFWYTLLYQAHREGIPVMRPLWVQYP QDVTTFNIDDQYLLGDALLVHPVSDSGAHGVQV YLPGQGEVWYDIQSYQKHHGPQTLYLPVTLSSIP VFQRGGTIVPRWMRVRRSSECMKDDPITLFVALS PQGTAQGELFLDDGHTFNYQTRQEFLLRRFSFSG NTLVSSSADPEGHFETPIWIERVVIIGAGKPAAVV LQTKGSPESRLSFQHDPETSVLVLRKPGINVASD WSIHLR
3849	A	1	1717	RARNARGCWGVCRSGFSSAVCGAARMEQVAEG ARVTAVPVSAADSTEELAEVEEGVGVVGEDNDA AARGAEAFGDSEEDGEDVFEVEKILDMKTEGGK VLYKVRWKGYTSDDDTWEPEIHLEDCKEVLLEF RKKIAENKAKAVRKDIQRLSLNNDIFEANSDSDQ QSETKEDTSPKKKKKKLRQREEKSPDDLKKKKA KAGKLKDKSKPDLESSLESLVFDLRTKKRISEAK EELKESKKPKKDEVKETKELKKVKKGEIRDLKT KTREDPKENRKTKKEKFVESQVESESSVLNDSPF PEDDSEGLHSDSREEKQNTKSARERAGQDMGLE HGFEKPLDSAMSAEEDTDVRGRRKKKTPRKAED TRENRKLENKNAFLEKKTVPKKQRNQDRSKSAA ELEKLMPVSAQTPKGRRLSGEERGLWSTDSAEE DKETKRNESKKPKKDEVKETKELKKVKKGEIRD LKTKTREDPKENRKTKKEKFVESQVESESSVLND SPFPEDDSEGLHSDSREEKQNTKSARERAGQDM GLEHGFEKPLDSAMSAEEDTDVRGRRKKKTPRK AEDTRENRKLENKNAFLEKKTVPKKQRNQDRSK SAAELEKLMPVSAQTPKGRRLSGEERGLWSTDS AEEDKETKRNESKKPKKDEVKETKELKKVKKGE

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				IRDLKTKTREDPKENRKTKKEKFVESQVESESSV LNDSPFPED/RQ*RATFRQQREEKSPDDLKKKKA KAGKLKDKSKPDLESSLESLVFDLRTKKRISEAK EELKESKKPK
3850	A	1113	3975	PAAAAAAAAAAAAAAGRGPSFTPCFSPSLAVEPS RRTRLGSDPAQAMAGNVKKSSGAGGGSGSGGS GSGGLIGLMKDAFQPHHHHHHHLSPHPPGTVDK KMVEKCWKLMDKVVRLCQNPKLALKNSPPYIL DLLPDTYQHLRTILSRYEGKMETLGENEYFRVF MENLMKKTKQTISLFKEGKERMYEENSQPRRNL TKLSLIFSHMLAELKGIFPSGLFQGDTFRITKADA AEFWRKAFGEKTIVPWKSFRQALHEVHPISSGLE AMALKSTIDLTCNDYISVFEFDIFTRLFQPWSSLL RNWNSLAVTHPGYMAFLTYDEVKARLQKFIHKP GSYIFRLSCTRLGQWAIGYVTADGNILQTIPHNKP LFQALIDGFREGFYLFPDGRNQNPDLTGLCEPTP QDHIKVTQEQYELYCEMGSTFQLCKICAENDKD VKIEPCGHLMCTSCLTSWQESEGQGCPFCRCEIK GTEPIVVDPFDPRGSGSLLRQGAEGAPSPNYDDD DDERADDTLFMMKELAGAKVERPPSPFSMAPQA SLPPVPPRLDLLPQRVCVPSSASALGTASKAASGS LHKDKPLPVPPTLRDLPPPPPPDRPYSVGAESRPQ RRPLPCTPGDCPSRDKLPPVPSSRLGDSWLPRPIP KVPVSAPSSSDPWTGRELTNRHSLPFSLPSQMEP RPDVPRLGSTFSLDTSMSMNSSPLVGPECDHPKI KPSSSANAIYSLAARPLPVPKLPPGEQCEGEEDTE YMTPSSRPLRPLDTSQSSRACDCDQQIDSCTYEA MYNIQSQAPSITESSTFGEGNLAAAHANTGPEES ENEDDGYDVPKPPVPAVLARRTLSDISNASSS/FG LFVLERDP*PQNVTEGSQVPERPPKPFPRRINSER KAGSCQQGSGPAASAATA\SPQLSSEIENLMSQG YSYQDIQKALVIAQNNIEMAKNILREFVSISSPAH VAT
3851	A	2	2781	GRVGSMDGAMGPRGLLLCMYLVSLLILQAMPA LGSATGRSKSSEKRQAVDTAVDGVFIRSLKVNC KVTSRFAHYVVTSQVVNTANEAREVAFDLEIPK TAFISDFAVTADGNAFIGDIKDKVTAWKQYRKA AISGENAGLVRASGRTMEQFTIHLTVNPQSKVTF QLTYEEVLKRNHMQYEIVIKVKPKQLVHHFEIDV DIFEPQGISKLDAQASFLPKELAAQTIKKSFSGKK GHVLFRPTVSQQQSCPTCSTSLLNGHFKVTYDVS RDKICDLLVANNHFAHFFAPQNLTNMNKNVVFV IDISGSMRGQKVKQTKEALLKILGDMQPGDYFD LVLFGTRVQSWKGSLVQASEANLQAAQDFVRGF SLDEATNLNGGLLRGIEILNQVQESLPELSNHASI LIMLTDGDPTEGVTDRSQILKNVRNAIRGRFPLY NLGFGHNVDFNFLEVMSMENNGRAQRIYEDHD ATQQLQGFYSQVAKPLLVDVDLQYPQDAVLALT QNHHKQYYEGSEIVVAGRIADNKQSSFKADVQA HGEGQEFSITCLVDEEMKKLLRERGHMLENHV ERLWAYLTIQELLAKRMKVDREVRANLSSQALR MSLDYGFVTPLTSMSIRGMADQDGLKPTIDKPSE DSPPLEMLGPRRTFVLSALQPSPTHSSSNTQRLPD RVTGVDTDPHFIIHVPQKEDTLCFNINEEPGVILS LVQDPNTGFSVNGQLIGNKARSPGQHDGTYFGR

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				LGIANPATDFQLEVTPQNITLNPGFGGPVFSWRD QAVLRQDGVVVTINKKRNLVVSVDDGGTF\EVV\ LHRVW\KGSS\VHQDFLGLLMCWDKSIGMSSPGR KGCWGQ\FFHPIRFLKVS*HPPPGSDPQKAQMPT MVVRNPPGLTVT\RGLQKDYSKDPWHGAEVSC WFI\HNNGA*I\TDCAYTDYI\VPDIF
3852	A	39	1735	TQVAEAGRGEGVVAGAETGRPQSAGMNLELLES FGQNYPEEADGTLDCISMALTCTFNRWGTLLAV GCNDGRIVIW\DF\LTRGIA*NKFSAHIHPVCSLC WSRDGHKLVSASTDNIVSQWDVLSGDCDQRFRF PSPILKVQYHPRDQNKVLVCPMKSAPVMLTLSD SKHVVLPVDDDSDLNVVASFDRRGEYIYTGNAK GKILVLKTDSQDLVASFRVTTGTSNTTAIKSIEFA RKGSCFLINTADRIIRVYDGREILTCGRDGEPEPM QKLQDLVNRTPWKKCCFSGDGEYIVAGSARQH ALYIWEKSIGNLVKILHGTRGELLLDVAWHPVRP IIASISSGVVSIWAQNQVENWSAFAPDFKELDEN VEYEERESEFDIEDEDKSEPEQTGADAAEDEEVD VTSVDPIAAFCSSDEELEDSKALLYLPIAPEVEDP EENPYGPPPDAVQTSLMDEGASSEKKRQSSADG SQPPKKKPKTTNIELQGVPNDEVHPLLGVKGDG KSKKKQAGRPKGSKGKEKDSPFKPKLYKGDRGL PLEGSAKGKVQAELSQPLTAGGAISELL
3853	A	45	2603	PLLFTCGREVRARDPEKEGTIVVAGLKVQVQPRF LWILCFSMEETQGELTSSCGSKTMANVSLAFRDV SIDLSQEEWECLDAVQRDLYKDVMLENYSNLVS LDLEYKYITKNLLSEKNVCKIYLSQLQTGEKSKN TIHEDTIFRNGLQCKHEFERQERHQMGCVSQMLI QKQISHPLHPKIHAREKSYECKECRKAFRQQSYLI QHLRIHTGERPYKCMECGKAFCRVGDLRVHHTI HAGERPYECKECGKAFRLHYHLTEHQRIHSGVK PYECKECGKAFSRVRDLRVHQTIHAGERPYECK ECGKAFRLHYQLTEHQRIHTGERPYECKVCGKT FRVQRHISQHQKIHTGVKPYKCNECGKAFSHGS YLVQHQKIHTGEKPYECKECGKSFSFHAELARH RRIHTGEKPYECRECGKAFRLQTELTRHHRTHTG EKPYECKECGKAFICGYQLTLHLRTHTGEIPYEC KECGKTFSSRYHLTQHYRIHTGEKPYICNECGKA FRLQGELTRHHRIHTCEKPYECKECGKAFIHSNQ FISHQRIHTSESTYICKECGKIFSRRYNLTQHFKIH TGEKPYICNECGKAFRFQTELTQHHRIHTGEKPY KCTECGKAFIRSTHLTQHHRIHTGEKPYECTECG KTFSRHYHLTQHHRGHTGEKPYICNECGNAFICS YRLTLHQRIHTGELPYECKECGKTFSRRYHLTQH FRLHTGEKPYSCKECGNAFRLQAELTRHHIVHTG EKPYKCKECGKAFSVNSELTRHHRIHTGEKPYQC KECGKAFIRSDQLTLHQ\KIILVR\NPMHNVKRIR WPLENAL*QRICNLRNFLFVTEHVGIPFTSCSQFI RNYFVC
3854	A	108	894	LQSCWVPGIPWPSVGWLSWLKDLPSCEIHSASLS AVLQGPQCSEMLWPKNLTSWDDSSSVSSGISDTI DNLSTDDINTSSSISSYANTPASSRKNLDVQTDAE KHSQVERNSLWSGDDVKKSDGGSDSGIKMEPGS KWRRNPSDVSDESDKSTSGKKNPVISQTGSWRR GMTAQVGITMPRTKASAPAGALKTPGTGKRPGL

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				S\GPGAPTPAAPPQLARMAWAFSLSAASTPAVSP STSPSAVEGSPATILPLASSPPPRTTP*LPLSELTV* RPQELVRGRGCLGPGAPTPAAPPQLARMAWAFS LSAASTPAVSPSTSPSAVEGSPATILPLASSPPPRT TP
3855	A	1	772	FRGGDGAPGVLKPGNPLPFPLPPLQYPPPSTLSHS DNLAMTSRSTARPNGQPQASKICQFKLVLLGESA VGKSSLVLRFVKGQFHEYQESTIGAAFLTQSVCL DDTTVKFEIWDTAGQERYHSLAPMYYRGAQAAI VVYDITNQETFARAKTWVKELQRQASP\SIVVGL AGNKADLANKRMVEYEEAQAYADDNSLLFMET SAKTAMNVNDLFL\AIA*EVAKRVNPQNLG\G\A AGRSRGVDLHEQS\QQNKSQCCSN
3856	A	2815	352	LGLEAAARPRPGGPAAMQDGNFLLSALQPEAGV CSLALPSDLQLDRRGAEGPEAERLRAARVQEQV RARLLQLGQQPRHNGAAEPEPEAETARGTSRGQ YHTLQAGFSSRSQGLSGDKTSGFRPIAKPAYSPA SWSSRSAVDLSCSRRLSSAHNGGSAFGAAGYGG AQPTPPMPTRPVSFHERGGVGSRADYDTLSLRSL RLGPGGLDDRYSLVSEQLEPAATSTYRAFAYER QASSSSSRAGGLDWPEATEVSPSRTIRAPAVRTL QRFQSSHRSRGVGGAVPGAVLEPVARAPSVRSLS LSLADSGHLPDVHGFNSYGSHRTLQRLSSGFDDI DLPSAVKYLMASDPNLQVLGAAYIQHKCYSDAA AKKQARSLQAVPRLVKLFNHANQEVQRHATGA MRNLIYDNADNKLALVEENGIFELLRTLREQDDE LRKNVTGILWNLSSSDHLKDRLAKKTPLE\QLT\D LGV*APLSGAGGPP\LIQQNASEAEIFYNATGFPR NLSSASQATRQKMRECHGLVDALVTSINHALDA GKCEDKSVENAVCVLRNLSYRLYDEMPPSALQR LEGRGRRDLAGAPPGEVVGCFTPQSRRLRELPLA ADALTFAEVSKDPKGLEWLWSPQIVGLYNRLLQ RCELNRHTTEAAAGALQNITGG\DPRGPGGLSRL ALEQERILNPLLDRVRTADHHQLRSLTGLIRNLS RNARNKDEMSTKVV\SHLI\EKLPGSVGEKSPPAE VLV\NI\IAVFNNLGWLASPI/ALARDLLYFDGLRK LIFIKKKRDSPDSEKSSRAASSLLANLWQYNKLH RDFRAKGYRKEDFLGP
3857	A	1034	204	VAVTLLSQLPSAIQRTAAWEMRAPLTFRVPLALD LIKPEHCTVNVDNSLSIPVIAAELVVRKPSEKGM QQKKKTKDLGFRAGKESKTEWRK*GLQDMASQ MFALPLK*PVTAAFHDSSMPSSLLQIEMEQLFLE ARLQ/PDSKSEARRNQCDSMLLRNQQLCSTCQE MKMVQPRTMKIPDDPKASFENCMSYRMSLHQP KFQTTPEPFHDDIPTENIHLQNL/PILGPRTAVFHG LLTEAYKTLKERQRSSLPRKEPIGKTTEAVSGRSS SPPRLPERK
3858	A	203	3469	SHQEIEQNSAMAPRKRGGRGISFIFCCFRNNDHPE ITYRLRNDSNFALQTMEPALPMPPVEELDVMFSE LVDELDLTDKHREAMFALPAEKKWQIYCSKKK DQEENKGATSWPEFYIDQLNSMAARKSLLALEK EEEEERSKTIESLKTALRTKPMRFVTRFIDLDGLS CILNFLKTMDYETSESRIHTSLIGCIKALMNNSQG RAHVLAHSESINVIAQSLSTENIKTKVAVLEILGA VCLVPGGHKKVLQAMLHYQKYASERTRFQTLIN

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				DLDKSTGRYRDEVSLKTAIMSFINAVLSQGAGVE SLDFRLHLRYE\FLMLGIHPVMDKLRKHENSTLD RHLDFFEMLRNEDELEFAKRFELVHIDTKSATQM FELTRKRLTHSEAYPHFMSILHHCLQMPYKRSGN TVQYWLLLDRIIQQIVIQNDKGQDPDSTPLENFNI KNVVRMLVNENEVKQWKEQAEKMRKEHNELQ QKLEKKERECDAKTQEKEEMMQTLNKMKEKLE KETTEHKQVKQQVADLTAQLHELSRRAVCASIP GGPSPGAPGGPFPSSVPGSLLPPPPPPPLPGGMLPP PPPPLPPGGPPPPPGPPPLGAIMPPPGAPMGLALK KKSIPQPTNALKSFNWSKLPENKLEGTVWTEIDD TKVFKILDLEDLERTFSAYQRQQDFFVNSNSKQK EADAIDDTLSSKLKVKELSVIDGRRAQNCNILLS RLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFV PEKSDIDLLEEHKHELDRMAKADRFLFEMSRINH YQQRLQSLYFKKKFAERVAEVKPKVEAIRSGSEE VFRSGALKQLLEVVLAFGNYMNKGQRGNAYGF KISSLNKIADTKSSIDKNITLLHYLITIVENKYPSV LNLNEELRDIPQAAKVNMTELDKEISTLRSGLKA VETELEYQKSQPPQPGDKFVSVVSQFITVASFSFS DVEDLLAEAKDLFTKAVKHFGEEAGKIQPDEFF GIFDQFLQAVSEAKQENENMRKKKEEEERRARM EAQLKEQRERERKMRKAKENSEESGEFDDLVSA LRSGEVFDKDLSKLKRNRKRITNQMTDSSRERPI TKLNF
3859	A	1279	141	RVEHLSEFLVDIKPSLTFDVIPLLDPYGPAGSDPS LEFLVVSEETYRGGMAINRFRLENDLEELALYQI QLLKDLRHTENEEDKVSSSSFRQRMLGNLLRPPY ERPELPTCLYVIGLTGISGSGKSSIAQRLKGLGAF VIDSDHLGHRAYAPGGPAYQPVVEAFGTDILHK DGIINRKVLGSRVFGNKKQLKILTDIMWPIIAKLA REEMDRAVAEGKRVCVIDAAVLLEAGWQNLVH EVWTAVIPETEAVRRIVERDGLSEAAAQSRLQSQ MSGQQLVEQSHVVLST\CGSRISPNARWRKPGPS CRSAFPRLIRPSTEKFSVGPDWLLELTSDPVVRRN GGLDAHPGSGPEVQAILCRTWPGLVDTGSLPNTL VFGQH
3860	A	1	3881	MGQKSVGASYVQIPLVPPLSRHPKGLGHEDRWS SYCLSSLAAQNICTSKLHCPAAPEHTDPSEPRGSV SCCSLLRGLSSGWSSPLLPAPVCNPNKAIFTVDA KTTEILVANDKACGLLGYSSQDLIGQKLTQFFLR SDSDVVEALSEEHMEADGHAAVVFGTVVDIISRS GEKIPVSVWMKRMRQERRLCCVVVLEPVERVST WVAFQSDGTVTSCDSLFAHLHGYVSGEDVAGQ HITDLIPSVQLPPSGQHIPKNLKIQRSVGRARDGT TFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWV FCTISGLITLLPDGTIHGINHSFALTLFGYGKTELL GKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDV GNESGCGERTLDPWQGQDPAEGGQDPRINVVLA GGHVVPRDEIRKLMESQDIFTGTQTELIAGGQLL SCLSPQPAPGVDNVPEGSLPVHGEQALPKDQQIT ALGREEPVAIESPGQDLLGESRSEPVDVKPFASCE DSEAPVPAEDGGSDAGMCGLCQKAQLERMGVS GPSGSDLWAGAAVAKPQAKGQLAGGSLLMHCP CYGSEWGLWWRSQDLAPSPSGMAGLSFGTPTLD

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				EPWLGVENDREELQTCLIKEQLSQLSLAGALDVP HAELVPTECQAVTAPVSSCDLGGRDLCGGCTGS SSACYALATDLPGGLEAVEAQEVDVNSFSWNLK ELFFSDQTDQTSSNCSCATSELRETPSSLAVGSDP DVGSLQEQGSCVLDDRELLLLTGTCVDLGQGRR FRESCVGHDPTEPLEVCLVSSEHYAASDRESPGH VPSTLDAGPEDTCPSAEEPRLNVQVTSTPVIVMR GAAGLQREIQEGAYSGSCYHRDGLRLSIQFEVRR VELQGPTPLFCCWLVKDLLHSQRDSAARTRLFL ASLPGSTHSTAAELTGPSLVEVLRARPWFEEPPK AVELEGLAACEGEYSQKYSTMSPLGSGAFGFVW TAVDKEKNKEVVVKFIKKEKVLEDCWIEDPKLG KVTLEIAILSRVEHANIIKVLDIFENQGFFQLVME KHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAG\Q SRLVSAVGYLRLKDIIHRDIKDENIVIAEDFTIKLI DFGSAAYLERGKLFYTFCGTIEYCAPEVLMGNPY RGPELEMWSLGVTLYTLVFEENPFCELEETVEAA IHPPYLVSKELMSLVSGLLQPVPERRTTLEKLVT DPWVTQPVNLADYTWEEVFRVNKPESGVLSAAS LEMGNRSLSDVAQAQELCGGPVPGEAPNGQGCL HPGDPRLLTS
3861	A	1	3881	MGQKSVGASYVQIPLVPPLSRHPKGLGHEDRWS SYCLSSLAAQNICTSKLHCPAAPEHTDPSEPRGSV SCCSLLRGLSSGWSSPLLPAPVCNPNKAIFTVDA KTTEILVANDKACGLLGYSSQDLIGQKLTQFFLR SDSDVVEALSEEHMEADGHAAVVFGTVVDIISRS GEKIPVSVWMKRMRQERRLCCVVVLEPVERVST WVAFQSDGTVTSCDSLFAHLHGYVSGEDVAGQ HITDLIPSVQLPPSGQHIPKNLKIQRSVGRARDGT TFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWV FCTISGLITLLPDGTIHGINHSFALTLFGYGKTELL GKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDV GNESGCGERTLDPWQGQDPAEGGQDPRINVVLA GGHVVPRDEIRKLMESQDIFTGTQTELIAGGQLL SCLSPQPAPGVDNVPEGSLPVHGEQALPKDQQIT ALGREEPVAIESPGQDLLGESRSEPVDVKPFASCE DSEAPVPAEDGGSDAGMCGLCQKAQLERMGVS GPSGSDLWAGAAVAKPQAKGQLAGGSLLMHCP CYGSEWGLWWRSQDLAPSPSGMAGLSFGTPTLD EPWLGVENDREELQTCLIKEQLSQLSLAGALDVP HAELVPTECQAVTAPVSSCDLGGRDLCGGCTGS SSACYALATDLPGGLEAVEAQEVDVNSFSWNLK ELFFSDQTDQTSSNCSCATSELRETPSSLAVGSDP DVGSLQEQGSCVLDDRELLLLTGTCVDLGQGRR FRESCVGHDPTEPLEVCLVSSEHYAASDRESPGH VPSTLDAGPEDTCPSAEEPRLNVQVTSTPVIVMR GAAGLQREIQEGAYSGSCYHRDGLRLSIQFEVRR VELQGPTPLFCCWLVKDLLHSQRDSAARTRLFL ASLPGSTHSTAAELTGPSLVEVLRARPWFEEPPK AVELEGLAACEGEYSQKYSTMSPLGSGAFGFVW TAVDKEKNKEVVVKFIKKEKVLEDCWIEDPKLG KVTLEIAILSRVEHANIIKVLDIFENQGFFQLVME KHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAG\Q SRLVSAVGYLRLKDIIHRDIKDENIVIAEDFTIKLI DFGSAAYLERGKLFYTFCGTIEYCAPEVLMGNPY

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				RGPELEMWSLGVTLYTLVFEENPFCELEETVEAA IHPPYLVSKELMSLVSGLLQPVPERRTTLEKLVT DPWVTQPVNLADYTWEEVFRVNKPESGVLSAAS LEMGNRSLSDVAQAQELCGGPVPGEAPNGQGCL HPGDPRLLTS
3862	A	399	2069	TMDRSKRNSIAGFPPRVE\RLEEFEGGGGGEGNV SQVGRVWPSSYRALISAFFRLTRLDDFTCEKIGSG FFSEVFKVRHRASGQVMALKMNTLSSNRANML KEVQLMNRLSHPNILRYINSGNLEQLLDSNLHLP WTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNC LIKRDENGYSAVVADFGLAEKIPDVSMGSEKLA VVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEII ARIQADPDYLPRTENFGLDYDAFQHMVGDCPPD FLQLTFNCCNMDPKLRPSFVEIGKTLEEILSRLQE EEQERDRKLQPTARGLLEKAPGVKRLSSLDDKIP HKSPCPRRTIWLSRSQSDIFSRKPPRTVSVLDPYY RPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSK SVISLVFDLDAPGPGTMPLADWQEPLAPPIRRWR SLPGSPEFLHQEACPFVGREESLSDGPPPRLSSLK YRVKEIPPFRASALPAAQAHEAMDCSILQEENGF GSRPQGTSPCPAGASEEMEVEERPAGSTPATFSTS GIGLQTQGKQDG
3863	A	399	2069	TMDRSKRNSIAGFPPRVE\RLEEFEGGGGGEGNV SQVGRVWPSSYRALISAFFRLTRLDDFTCEKIGSG FFSEVFKVRHRASGQVMALKMNTLSSNRANML KEVQLMNRLSHPNILRYINSGNLEQLLDSNLHLP WTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNC LIKRDENGYSAVVADFGLAEKIPDVSMGSEKLA VVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEII ARIQADPDYLPRTENFGLDYDAFQHMVGDCPPD FLQLTFNCCNMDPKLRPSFVEIGKTLEEILSRLQE EEQERDRKLQPTARGLLEKAPGVKRLSSLDDKIP HKSPCPRRTIWLSRSQSDIFSRKPPRTVSVLDPYY RPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSK SVISLVFDLDAPGPGTMPLADWQEPLAPPIRRWR SLPGSPEFLHQEACPFVGREESLSDGPPPRLSSLK YRVKEIPPFRASALPAAQAHEAMDCSILQEENGF GSRPQGTSPCPAGASEEMEVEERPAGSTPATFSTS GIGLQTQGKQDG
3864	A	3	911	SWNMDSDSCAAAFHPEEYSPSCKRRRTVEDFNK FCTFVLAYAGYIPYPKEELPLRSSPSPANSTAGTI DSDGWDAGFSDIASSVPLPVSDRCFSHLQPTLLQ RAKPSNFLLDRKKTDKLKKKKRKRRDSDAPGK EGYRGGLLKLEAADPYVETPTSPTLQDIPQAPSD PCSGWDSDTPSSGSCATVSPDQVKEIKTEGKRTI VR/QEAQLMARNDGNFSSLLESIFPS\DDDSWDLV TCFCMKPFAGRPMIECNECHTWIHLSCAKIRKSN VPEVFVCQKCRDSKFDIRRSNRSRTGSRKLFLD
3865	A	3	3573	QERLRSRSRPDRAAREAGSARGRQPKRTERVEQ FLTIARRRGRRSMPVSLEDSGEPTSCPATDAETAS EGSVESASETRSGPQSASTAVKERPASSEKVKGG DDHDDTSDSDSDGLTLKELQNRLRRKREQEPTE RPLKGIQSRLRKKRREEGPAETVGSEASDTVEGV LPSKQEPENDQGVVSQAGKDDRESKLEGKAAQD IKDEEPGDLGRPKPECEGYDPNALYCICRQPHNN

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				RFMICCDRCEEWFHGDCVGISEARGRLLERNGE DYICPNCTILQVQDETHSETADQQEAKWRPGDA DGTDCTSIGTIEQKSSEDQGIKGRIEKAANPSGKK KLKIFQPGPGPVPTQLPVLWQVLEIAVSRSISAFT LLHCISCKVIEAPGASKCIGPGCCHVAQPDSVYCS NDCILKHAAATMKFLSSGKEQKPKPKEKMKMK PEKPSLPKCGAQAGIKISSVHKRPAPEKKETTVK KAVVVPARSEALGKEAACESSTPSWASDHNYNA VKPEKTAAPSPSLLYKSTKEDRRSEEKAAATAAS KKTAPPGSTVGKQPAPRNLVPKKSSFANVAAAT PAIKKPPSGFKGTIPKRPWLSATPSSGASAARQAG PAPAAATAASKKFPGSAALVGAVRKPVVPSVPM ASPAPGRLGAMSAAPSQPNSQIRQNIRRSLKEIL WK/RFLFFILFRVNDSDDLIMTENEVGKIALHIEK EMFNLFQVTDN/RAYKSKYRSIMFNLKDPKNQG LFHRVLREEISLAKLVRLKPEELVSKELSTWKER PARSVMESRTKLHNESKKTAPRQEAIPDLEDSPP VSDSEEQQESARAVPEKSTAPLLDVFSSMLKDTT SQHRAHLFDLNCKICTGQVPSAEDEPAPKKQKLS ASVKKEDLKSKHDSSAPDPAPDSADEVMPEAVP EVASEPGLESASHPNVDRTYFPGPPGDGHPEPSPL EDLSPCPASCGSGVVTTVTVSGRDPRTAPSSSCT AVASAASRPDSTHMVEARQDVPKPVLTSVMVPK SILAKPSSSPDPRYLSVPPSPNISTSESRSPPEGDTT LFLSRLSTIWKGFINMQSVAKFVTKAYPVSGCFD YLSEDLPDTIHIGGRIAPKTVWDYVGKLKSSVSK ELCLIRFHPATEEEEVAYISLYSYFSSRGRFGVVA NNNRHVKDLYLIPLSAQDPVPSKLLPFEGPGKRR LSGWR
3866	A	2	3181	AQQPVGRRGGASGAGGGRRGTPRPRAGAGPGF QVSSGGCRLSKMRRFLRPGHDPVRERLKRDLFQ FNKTVEHGFPHQPSALGYSPSLRILAIGTRSGAIK LYGAPGVEFMGLHQENNAVTQIHLLPGQCQLVT LLDDNSLHLWSLKVKGGASELQEDESFTLRGPP GAAPSATQITVVLPHSSCELLYLGTESGNVFVVQ LPAFRALEDRTISSDAVLQRLPEEARHRRVFEMV EALQEHPRDPNQILIGYSRGLVVIWDLQGSRVLY HFLSSQQLENIWWQRDGRLLVSCHSDGSYCQWP VSSEAQQPEPLRSLVPYGPFPCKAITRILWLTTRQ G\LPFTIFQGGMPRASYGDRHCISVIHDGQQTAFD FTSRVIGFTVLTEADPAATFDDPYALVVLAEEEL VVIDLQTAGWPPVQLPYLASLHCSAITCSHHVSN IPLKLWERIIAAGSRQNAHFSTMEWPIDGGTSLTP APPQRDLLLTGHEDGTVRFWDASGVCLRLLYKL STVRVFLTDTDPNENLSAQGEDEWPPLRKVGSF DPYSDDPRLGIQKIFLCKYSGYLAVAGTAGQVLV LELNDEAAEQAVEQVEADLLQDQEGYRWKGHE RLAARSGPVRFEPGFQPFVLVQCQPPAVVTSLAL HSEWRLVAFGTSHGFGLFDHQQRRQVFVKCTLH PSDQLALEGPLSRVKSLKKSLRQSFRRMRRSRVS SRKRHPAGPPGEAQEGSAKAERPGLQNMELAPV QRKIEARSAEDSFTGFVRTLYFADTYLKDSSRHC PSLWAGTNGGTIYAFSLRVPPAERRMDEPVRAE QAKEIQLMHRAPVVGILVLDGHSVPLPEPLEVAH DLSKSPDMQGSHQLLVVSEEQFKVFTLPKVSAK

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				LKLKLTALEGSRVRRVSVAHFGSRRAEDYGEHH LAVLTNLGDIQVVSLPLLKPQVRYSCIRREDVSGI ASCVFTKYGQGFYLISPSEFERFSLSTKG\LVEPRC LVDSAETKNHRPGNGAGPKKAPSRARNSGTQSD GEEKQPGLVMERALLSDERAATG\VHIEPPWGA ASAMAEQSEWLSVQAAR
3867	A	2	3181	AQQPVGRRGGASGAGGGRRGTPRPRAGAGPGF QVSSGGCRLSKMRRFLRPGHDPVRERLKRDLFQ FNKTVEHGFPHQPSALGYSPSLRILAIGTRSGAIK LYGAPGVEFMGLHQENNAVTQIHLLPGQCQLVT LLDDNSLHLWSLKVKGGASELQEDESFTLRGPP GAAPSATQITVVLPHSSCELLYLGTESGNVFVVQ LPAFRALEDRTISSDAVLQRLPEEARHRRVFEMV EALQEHPRDPNQILIGYSRGLVVIWDLQGSRVLY HFLSSQQLENIWWQRDGRLLVSCHSDGSYCQWP VSSEAQQPEPLRSLVPYGPFPCKAITRILWLTTRQ G\LPFTIFQGGMPRASYGDRHCISVIHDGQQTAFD FTSRVIGFTVLTEADPAATFDDPYALVVLAEEEL VVIDLQTAGWPPVQLPYLASLHCSAITCSHHVSN IPLKLWERIIAAGSRQNAHFSTMEWPIDGGTSLTP APPQRDLLLTGHEDGTVRFWDASGVCLRLLYKL STVRVFLTDTDPNENLSAQGEDEWPPLRKVGSF DPYSDDPRLGIQKIFLCKYSGYLAVAGTAGQVLV LELNDEAAEQAVEQVEADLLQDQEGYRWKGHE RLAARSGPVRFEPGFQPFVLVQCQPPAVVTSLAL HSEWRLVAFGTSHGFGLFDHQQRRQVFVKCTLH PSDQLALEGPLSRVKSLKKSLRQSFRRMRRSRVS SRKRHPAGPPGEAQEGSAKAERPGLQNMELAPV QRKIEARSAEDSFTGFVRTLYFADTYLKDSSRHC PSLWAGTNGGTIYAFSLRVPPAERRMDEPVRAE QAKEIQLMHRAPVVGILVLDGHSVPLPEPLEVAH DLSKSPDMQGSHQLLVVSEEQFKVFTLPKVSAK LKLKLTALEGSRVRRVSVAHFGSRRAEDYGEHH LAVLTNLGDIQVVSLPLLKPQVRYSCIRREDVSGI ASCVFTKYGQGFYLISPSEFERFSLSTKG\LVEPRC LVDSAETKNHRPGNGAGPKKAPSRARNSGTQSD GEEKQPGLVMERALLSDERAATG\VHIEPPWGA ASAMAEQSEWLSVQAAR
3868	A	1	2497	GDSGGPLVCEEPSGRFFLAGIVSWGIGCAEARRP GVYARVTRLRDWILEATTKASMPLAPTMAPAPA APSTAWPTSPESPVVSTPTKSMQALSTVPLDWVT VPKLQECGARPAMEKPTRVVGGFGAASGEVPW QVSLKEGSRHFCGATVVGDRWLLSAAHCFNHT KVEQVRAHLGTASLLGLGGSPVKIGLRRVVLHP LYNPGILDFDLAVLELASPLAFNKYIQPVCLPLAI QKFPVGRKCMISGWGNTQEGNATKPELLQKASV GIIDQKTCSVLYNFSLTDRMICAGFLEGKVDSCQ VSGIKALYESELADARRVLDETARERARLQIEIG KLRAELDEVNKSAKKREGELTVAQGRVKDLESL FHRSEVELAAALSDKRGLESDVAELRAQLAKAE DGHAVAKKQLEKETLMRVDLENRCQSLQEELDF RKSVFEEEVVRETRRRHERRLVEVDSSRQQEYDFK MAQALEELRSQHDEQVRLYKLELEQTYQAKLDS AKLSSDQNDKAASAAREELKEARMRLESLSYQL SGLQKQASAAEDRIRELEEAMAGERDKFRKMLD

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				AKEQEMTEMRDVMQQQLAEYQELLDVKLALD MEINAYRKLLEGEEERLKLSPSPSSRVTVSRATSS SSGSLSATGRLGRSKRKR\WRWRSPW\QRPKRPG HGHGWQRWLPPGPAGLGLGQR\HIEEIDLEGKFV QLKNNSDKDQSLGNWRIKRQVLEGEEIAYKFTP KYILRAGQMVTVWAAGAGVAHSPPSTLVWKGQ SSWGTGESFRTVLVNADGEEVAMRTVKKSSVM RENENGEEEEEEAEFGEEDLFHQQGDPRTTSRGC YVM
3869	A	1	1942	RYRAGIPGDGRKDYIRLTRPGLTLPGRAMFARGS RRRRSGRAPPEAEDPDRGQPCNSCREQCPGFLLH GWRKICQHCKCPREEHAVHAVPVDLERIMCRLIS DFQRHSISDDDSGCASEEYAWVPPGLKPEQVYQ FFSCLPEDKVPYVNSPGEKYRIKQLLHQLPPHDS EAQYCTAL\EE\EEKKELRAFSQQRKRENLG/RLG IVRIFPVTIT\GAI\CEECGKQIGGGDIAVF\ASRASL GLLLGQPSCF\VCTTCQELLVDLIYFYHVGKVYC GRHHAECLRPRCQACDEIIFSPECTEAEGRHWHM DHFCCFECEASLGGQRYVMRQSRPHCCACYEAR HAEYCDGCGEHIGLDQGQMAYEGQHWHASDRC FCCSRCGRALLGRPFLPRRGLIFCSRACSLGSEPT APGPSRRSWSAGPVTAPLAASTASFSAVKGASET TTKGTSTELAPATGPEEPSRFLRGAPHRHSMPEL GLRSVPEPPPESPGQPNLRPDDSAFGRQSTPRVSF RDPLVSEGGPRRTLSAPPAQRRRPRSPPPRAPSRR RHHHHNHHHHHNRHPSRRRHYQCDAGSGSDSE SCSSSPSSSSSESSEDDGFFLGERIPLPPHLCRPMP AQDTAMETFNSPSLSLPRDSRAGMPRQARDKNC IVA
3870	A	2	3485	FVWRVFYVHASCMPPRARSWEGAHAPVGMHV AEAHACSSQQQQMPPAQFWMLEWLLHLCAFLS TPSFPHWCCCSNPHGSIADKPEEIVPASKPSRAAE NMAVEPRVATIKQRPSSRCFPAGSDMNSVYERQ GIAVMTPTVPGSPKAPFLGIPRGTMRRQKSIDSRI FLSGITEEERQFLAPPMLKFTRSLSMPDTSEDIPPP PQSVPPSPPPPSPTTYNCPKSPTPRVYGTIKPAFNQ NSAAKVSPATRSDTVATMMREKGMYFRRELDR YSLDSEDLYSRNAGPQANFRNKRGQMPENPYSE VGKIASKAVYVPAKPARRKGMLVKQSNVEDSPE KTCSIPIPTIIVKEPSTSSSGKSSQGSSMEIDPQAPE PPSQLRPDESLTVSSPFAAAIAGAVRDREKRLEA RRNSPAFLSADLGDEHVGLGPPAPRTRPSMFPEE GDFADEDSAEQLSSPMPSATPREPENHFVGGAEA SAPGEAGRPLNSTSKAQGPESSPAVPSASSGTAG PGNYVHPLTGRLLDPSSPLALALSARDRAMKES QQGPKGEAPKADLNKPLYIDTKMRPSLDAGFPT VTRQNTRGPLRRQETENKYETDLGRDRKGDDK KNMLIDIMDTSQQKSAGLLMVHTVDATKLDNA LQEEDEKAEVEMKPDSSPSEVPEGVSETEGALQI SAAPEPTTVPGRTIVAVGSMEEAVILPFRIPPPPLA SVDLDEDFIFTEPLPPPLEFANSFDIPDDRAASVPA LSDLVKQKKSDTPQSPSLNSSQPTNSADSKKPAS LSNCLPASFLPPPESFDAVADSGIEEVDSRSSSDH HLETTSTISTVSSISTLSSEGGENVDTCTVYADGQ AFMVDKPPVPPKPKMKPIIHKSNALYQDALVEE

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				DVDSFVIPPPAPPPPPGSAQPGMAKVLQPRTSKL WGDVTEIKSPILSGPKANVISELNSILQQMNREKL AKPGEGLDSPMGAKSASLAPRSPEIMSTISGTRST TVTFTVRPGTSQPITLQSRPPDYESRTSGTRRAPS PVVSPTEMNKETLPAPLSAATASPSPALSDVFSLP SQPPSGDLFGLNPAGRSRSPSPSILQQPISNKPFTT KPVHLWTKPDVADWLESLNLGEHKEAFMDNEI DGSHLPNLQKEDLIDLGVTRVGHRMNIERALKQ LLDR
3871	A	35	1171	VESRSAWHEGEDQIDRLDFIRNQMNLLTLDVKK KIKEVTEEVANKVSCAMTDEICRLSVLVDEFCSE FHPNPDVLKIYKSELNKHIEDGMGRNLADRCTD EVNALVLQTQQEIIENLKPLLPAGIQDKLHTLIPC KKFDLSYNLNYHKLCSDFQEDIVFRFSLGWSSLV HRFLGPRNAQRVLLGLSEPIFQLPRSLASTPTAPT TPATPDNASQEELMITLVTGLASVTSRTSMGIIIV GGVIWKTIGWKLLSVSLTMYGALYLYERLSWTT HAKERAFKQQFVNYATEKLRMIVSSTSANCSHQ VKQQIATTFARLCQQVDITQKQLEEEIARLPKEID QLEKIQNNSKLLRNKAVQLENELENFTKQFLPSS NEES
3872	A	35	1171	VESRSAWHEGEDQIDRLDFIRNQMNLLTLDVKK KIKEVTEEVANKVSCAMTDEICRLSVLVDEFCSE FHPNPDVLKIYKSELNKHIEDGMGRNLADRCTD EVNALVLQTQQEIIENLKPLLPAGIQDKLHTLIPC KKFDLSYNLNYHKLCSDFQEDIVFRFSLGWSSLV HRFLGPRNAQRVLLGLSEPIFQLPRSLASTPTAPT TPATPDNASQEELMITLVTGLASVTSRTSMGIIIV GGVIWKTIGWKLLSVSLTMYGALYLYERLSWTT HAKERAFKQQFVNYATEKLRMIVSSTSANCSHQ VKQQIATTFARLCQQVDITQKQLEEEIARLPKEID QLEKIQNNSKLLRNKAVQLENELENFTKQFLPSS NEES
3873	A	2944	2089	PVCTALTPGRMTDDKDVLRDVWFGRIPTCFTLY QDEITEREAEPYYLLLPRVSYLTLVTDKVKKHFQ KVMRQEDISEIWFEYEGTPLKWHYPIGLLFDLLA SSSALPWNITVHFKSFPEKDLLHCPSKDAIEAHF MSCMKEADALKHKSQVINEMQKKDHKQLWMG LQNDRFDQFWAINRKLMEYPAEENGFRYIPFRIY QTTTERPFIQKLFRPVAADGQLHTLGDLLKEVCP SAIDPEDGEKKNQVMIHGIEPMLETPLQWLSEHL SYPDNFLHISIIPQPTD
3874	A	776	366	QARGAPSSPMCPLPLAAAAVAAPRAPLRLLNRG LAAAMSTAQSLKSVDYEVFGRVQGVCFRMYTE DEARKIGVVGWVKNTSKGTVTGQVQGPEDKVN SMKSWLSKVGSPSSRIDRTNFSNEKTISKLEYSNF SIRY
3875	A	1081	182	SLSSCQTDPRPMSAPLDAALHALQEEQARLKMR LWDLQQLRKELGDSPKDKVPFSVPKIPLVFRGHT QQDPEVPKSLVSNLRIHCPLLAGSALITFDDPKVA EQVLQQKEHTINMEECRLRVQVQPLELPMVTTIQ VMVSSQLSGRRVLVTGFPASLRLSEEELLDKLEIF FGKTRNGGGDVDVRELLPGSVMLGFARDGVAQ RLCQIGQFTVPLGGQQVPLRVSPYVNGEIQKAEI RSQPVPRSVLVLNIPDILDGPELHDVLEIHFQKPT

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				RGGGEVEALTVVPQGQQGLAVFTSESG
3876	A	26	431	RMMKCPQALLAIFWLLLSWVSSEDKVVQSPLSL VVHEGDTVTLNCSYEVTNFRSLLWYKQEKKAPT FLFMLTSSGIEKKSGRLSSILDKKELSSILNITATQ TGDSAIYLCAVEAQCSLVTCSLYSNSTAEALQL
3877	A	3	1291	KAFRLLAERGAAAAMLWSGCRRFGARLGCLPG GLRVLVQTGHRSLTSCIDPSMGLNEEQKEFQKV AFDFAAREMAPNMAEWDQKELFPVDVMRKAA QLGFGGVYIQTDVGGSGLSRLDTSVIFEALATGC TSTTAYISIHNMCAWMIDSFGNEEQRHKFCPPLC TMEKFASYCLTEPGSGSDAASLLTSAKKQGDHYI LNGSKAFISGAGESDIYVVMCRTGGPGPKGISCIV VEKGTPGLSFGKKEKKVGWNSQPTRAVIFEDCA VPVANRIGSEGQGFLIAVRGLNGGRINIASCSLGA AHASVILTRDHLNVRKQFGEPLASNQYLQFTLA DMATRLVAARLMVRNAAVALQEERKDAVALCS MAKLFATDECFAICNQALQMHGGYGYLKDYAV QQYVRDSRVHQILEGSNEVMRILISRSLLQE
3878	A	10	1014	LPGSTISSSGCQAPGRADSSGGARNSRRGDSRPG SCNRQAVAPPCPSPGPQSRHWIHRGTAPQAGETR TLGRGSSAPNACSASVTPCCPSSPPS*SCL*PTRRS PQNSSSTEVYRGFWQHGLPST**PFSS*QWPGQH TQGCSKLLGKQTTHLPCSTWPA**PSPSCLTRFR* W*PSLMCLWASSCSVCV*SPSGSCRH*LWGTHST SRTC*ARRSSALPTGLCTDDTSWASSSKARPCAL QRPSSLSSLSPCLTC*W*LSSSSPMSARSPAGAET GSWATGSPRLTQWKSSRLTSTSHSARSAWKPSA TESTPSWPRFSSWTSGEDPASPAPAI
3879	A	200	699	LLLTGYIQTLQNQQLSGNQQEMQAVDNLTSAPG NTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLA MRIFFQIRSKSNFIIFLKNTVISDLLMILTFPFKILS DAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLIT IDRYQKTTRPFKTSNPKNLLGAKILK
3880	A	26	169	QPETDTMVHLTPEEKSAVTALWGKVNVDEDAG DDLCQILVDRPRLRI
3881	A	37	1100	TPLFDFWPGFVLSWLQPLSASLRARRAASGPPAC RIMPTTVDDVLEHGGEFHFFQKQMFFLLALLSAT FAPIYVGIVFLGFTPDHRCRSPGVAELSLRCGWSP AEELNYTVPGPGPAGEASPRQCRRYEVDWNQST FDCVDPLASLDTNRSRLPLGPCRDGWVYETPGSS IVTEFNLVCANSWMLDLFQSSVNVGFFIGSMSIG YIADRFGRKLCLLTTVLINAAAGVLMAISPTYTW MLIFRLIQGLVSKAGWLIGYILITEFVGRRYRRTV GIFYQVAYTVGLLVLAGVAYALPHWRWLQFTV ALPNFFFLLYYWCIPESPRWLISQNKNAEAMRIIK HIAKKNGKSLPASL
3882	A	573	1620	KSKCRFPEGLSEGFGPMRKEALSSGSVQEAEAM LDEPQEQAEGSLTVYVISEHSSLLPQDMMSYIGP KRTAVVRGIMHREAFNIIGRRIVQVAQAMSLTED VLAAALADHLPEDKWSAEKRRPLKSSLGYEITFS LLNPDPKSHDVYWDIEGAVRRYVQPFLNALGAA GNFSVDSQILYYAMLGVNPRFDSASSSYYLDMH SLPHVINPVESRLGSSAASLYPVLNFLLYVPELAH SPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDS KTYNASVLPVRVEVDMVRVMEVFLAQLRLLFGI

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				AQPQLPPKCLLSGPTSEGLMTWELDRLLWARSV ENLATATTLTSLA
3883	A	2369	844	RIHREEDFQFILKGIARLLSNPLLQTYLPNSTKKIQ FHQELLVLFWKLCDFNKVGQPRGALQGDGEQLP Q*PGGRDSVRLRGVGQSCPSLELSPLGPSPHP*KF LFFVLKSSDVLDILVPILFFLNDARADQSRVGLM HIGVFILLLLSGECNFGVRLNKPYSIRVPMDIPVF TGTHADLLIV\VFHKIITSGHQRLQPLFDCLLTIVV NVSPYLKSLSMVTANKLLHLLEAFSTTWFLFSAA QNHHLVFFLLEVFNNIIQYQFDGNSNLVYAIIRKR SIFHQLANLPTDPPTIHKALQRRRRTPEPLSRTGS QGGAPPWRAPAPLPLQSQAPSRPVWWLLQALTS *PRSPRCQRMAPCGPWNLSPSRAWRMAARLRGS PARHGGSSGDRP/HSSASGQWSPTPEWVLSWKS KLPLQTIMRLLQVLVPQVEKICIDKGLTDESEILR FLQHGTLVGLLPVPHPILIRKYQANSGTAMWFRT YMWGVIYLRNVDPPVWYDTDVKLFEIQRV
3884	A	1	804	NGPRAPFSQEGQSTGPPPLIPRLGQHGAQGRIPPL NPGQGPGPNKDDSRGPPNHHMGPMSERRHEQSG GPEHGPERGPLRGGQDCRGPPDRRGPHPDFPDDF SRPDDFHPDKRFGHRLREFEGRGGPLPQEEKWR RGGPGPPFPPDHREFSEGDGRGAARGPPGAWEG RRPGG*TFPPGSRGPTFS/SGAEEESFRRGAPPRHE GRAPPRGRDGFPGPEDFGPEENFDASEEAARGRD LRGRGRGTPRGERVTKDTWSGRIGCRIHWL
3885	A	3	996	GRRRAGPAHSARMYNMMETELKPPGPQQTSGG GGGNSTAAAAGGNQKNSPDRVKRPMNAFMVW SRGQRRKMAQENPKMHNSEISKRLGAEWKLLSE TEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTK TLMKKDKYTLPGGLLAPGGNSMASGVGVGAGL GAGVNQRMDSYAHMNGWSNGSYSMMQDQLG YPQHPGLNAHGAAQMQPMHRYDVSALQYNSM TSSQTYMNG/SRPTYSMSYSQQGTPGMAPGS\MG SVVKSEASSSPPVVTSSSHSRAPCQAGDLRDMIS MYLPGAEVPEPAAPSRLHMSQHYQSGPVPGTAI NGTLPLSHM
3886	A	773	317	QCTQKAAEGYTQFYYVDVLDGKLACVNKCTKG TKSQMNCNLGTCQLQRSGPRCLCPNTNTHWYW GETCEFNIAKSLVYGIVGAVMAVLLLALIILIILFS LSQ\RKRHRPESEGEADFGLENATNNFG\PTLETV DSGTELHIQ\RPEMVASTV
3887	A	3	466	VDFRVKTLLVDNKCFVLQLWDTAGQERYHSMT RQLLRKADGVVLMYDITSQESFAHVRYWLDCL QDAGSDGVVILLLGNKMDCEEERQVSVEAGQQL AQELGVYFGECSAALGHNILEPVVNLARSLRMQ EEGLKDSLVKVAPKRPPKRFGCCS
3888	A	3412	3144	QNIDITNFSSSWNDGLAFCALLHTYLPAHIPYQEL NSQDKRRNFMLAFQAAESVGIKSTLDINEMVRT ERPDWQNVMLYVTAIYKYFET
3889	A	1	1160	LVVTAITAILAFPNEYTRMSTSELISELFNDCGLL DSSKLCDYENRFNTSKGGELPDRPAGVGVYSAM WQLALTLILKIVITIFTFGMKIPSGLFIPSMAVGAI AGRLLGVGMEQLAYYHQEWTVFNSWCSQGAD CITPGLYAMVGAAACLGGVTRMTVSLVVIMFEL TGGLEYIVPLMAAAMTSKWVADALGREGIYDA

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				HIRLNGYPFLEAKEEFAHKTLAMDVMKPRRNDP LLTVLTQDSMTVEDVETIISETTYSGFPVVVSRES QRLVGFVLRRDLIISIENARKKQDGVVSTSIIYFTE HSPPLPPYTPPTLKLRNILDLSPFTVTDLTPMEIVV DIFRKLGLRQCLVTHNGRLLGIITKKDVLKHIAQ MANQDPDSILFN
3890	A	1	387	SWCWTGIFVLGTTNLRLEGSWYRSLWGPGFNTT TATLGFGAPQAPVGDVALNQPDMCVYRRGRKK RVPYTKLQLKELENEYAINKFINKDKRRRISAAT NLSERQVTIWFQNRRVKDKKIVSKLKDTVS
3891	A	2	2914	RGGGGDHKMADLSLLQEDLQEDADGFGVDDYS SESDVIIIPSALDLAST/QDEMVERPLGRL\DK\YA ASENHI*PDKMVAPEFASIPLRE\VCDDERDCIAV LGKN*PDWADDSEPT\VRAAELEQVPHIALFLFK KTRLSITICFFSKFLLPYCGLDTLADQN\NQVRKT SQAALL\ALLEQELIERFDVETKVCPVLIELTAPDS NDDVKTEAVAIMCKMAP\MVGKDITERLILPRFC EMCCDCRMFH\VRK\VCAANFGDICSVVGQQAT EEMLLPRFFQLCSDNVWGVRKACAECFMAVSC ATCQEIRRTKLSALFINLISDPSRWVRQAAFQSLG PFISTFANPSSSGQYFKEESKSSEEMSVENNKRTR DQEAPEDVQVRPEDTPSDLSVSNSSVILENTMED HAAEASGKPLGEISVPLDSSLLCTLSSESHQEAAS NENDKKPGNYKSMLRPEVGTTSQDSALLDQELY NSFHFWRTPLPEIDLDIELEQNSGGKPSPEGPEEE SEGPVPSSPNITMATRKELEEMIENLEPHIDDPDV KAQVEVLSAALRASSLDAHEETISIEKRSDLQDE LDINELPNCKINQEDSVPLISDAVENMDSTLHYIH NDSDLSNNSSFSPDEERRTKVQDVVPQALLDQY LSMTDPSRAQTVDTEIAKHCAYSLPGVALTLGR QNWHCLRETYETLASDMQWKVRRTLAFSIHELA VILGD\QLTAADLVPIFNGFLK*PSMKSRIGVLKH LHDFLKLLHIDKRREYLYQLQEFLVTDNSRNWR FRAELAEQLILLLELYSPRDVYDYLRPIALNLCAD KVSSVRWISYKLVSEMVKKLHAATPPTFGVDLIN ELVENFGRCPKWSGRQAFVFVCQTVIEDDCLPM DQFAVHLMPHLLTLANDRVPNVRVLLAKTLRQT LLEKDYFLASASCHQEAVEQTIMALQMDRDSDV KYFASIHPASTKISEDAMSTASSTY
3892	A	158	2191	VPLPAPSGLSGGGSRGAGCKKAPPGRAPAPGLAP LRPSEPTMAVPPGHGPFSGFPGPQEHTQVLPDVR LLPRRLPLAFRDATSAPLRKLSVDLIKTYKHINEV YYAKKKRRAQQAPPQDSSNKKEKKVLNHGYDD DNHDYIVRSGERWLERYEIDSLIGKGSFGQVVKA YDHQTQELVAIKIIKNKKAFLNQAQIELRLLELM NQHDTEMKYYIVHLKRHFMFRN\HLCLVFELLS YNLYDLLRNTHFRGVSLNLTRKLAQQLCTALLF LATPELSIIHCDLKPENILLCNPKRSAIKIVDFGSS CQLGQRIYQYIQSRFYRSPEVLLGTPYDLAIDMW SLGCILVEMHTGEPLFSGSNEVCPQEGVDQMNRI VEVLGIPPAAMLDQAPKARKYFERLPGGGWTLR RTKELRKDYQGPGTRRLQEVLGVQTGGPGGRRA GEPGHSPAD\Y\LRFQDLVLRMLEYEPAARISPLG ALQHGFFRRTADEATNTGPAGSSASTSPAPLDTC PSSSTASSISSSGGSSGSSSDNRTYRYSNRYCGGP

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				GPPITDCEMNSPQVPPSQPLRPWAGGDVPHKTH QAPASASSLPGTGAQLPPQPRYLGRPPSPTSPPPP ELMDVSLVGGPADCSPPHPAPAPQHPAASALRT RMTGGRPPLPPPDDPATLGPHLGLRGVPQSTAAS S
3893	A	68	258	PEEYYPFSPTLQQLFFFLLDSDMGSRPESMGCRK NTVPRPASPTEAGTDPQTFLHTWVSECRD
3894	A	1120	136	SLPLAPAPAVAGPVALCPAGLCPAQPGMPAGPA AASGSHPEVGSVLQRSSQPHWPNPWPGAGHLPP PAGPFPYNPPAGPGAAAGLA*SPPRSSPTPCSVGP QSCPANASAPPAQPCLAGAPPAASLPPPGPGSVS AAPAPGGPAPAEPPLGVPPVPAWLLPDSPPLPGT HSGPPPAAVSLPPAAAACPVVVPPPLPHHPPDLES PSAAAPNPGCAGGIRHFPPGSPEASSPLRPAAAPA LLPLPRPPS*P/VPWKPLHSPVAVAGGSFVAGGSV LPAPDLDQPRPSGPPAASPTPGPGVAQPPPGSAVL PTVP*APPVSGAAPGRKREW
3895	A	2	1347	FGAVSYRPGNGSCWVKVTASSDLSDLISCLCPPR SLCSSQACVLPVPGPSLLLPQGLHVGCASAGTRW PLSCSIDFQRLLAHEEETQKRRAKESGMAFTQLT FRDVAIEFSQDEWKCLNSTQRTLYRDVMLENYR NLVSLDLSRNCVIKELAPQQEGNP/ARSIPHSDIGT T*KT*H*RVLLQGNQEKNTRL*LSVER**KKLQQ SDYGPKRKSYL*ERPTR*KRYRKQVY*TSA*LSF LPHPHELQQFQAEGKIYECNHVEKSVNHGSSVSP PQIISSTIKTHVSNKYGTDFICSSLLTQEQKSCIRE KPYRYIECDKALNHGSHMTVRQVSHSGEKGYKC DLCGKVFSQKSNLARHWRVHTGEKPYKCNECD RSFSRNSCLALHRRVHTGEKPYKCYECDKVFSR NSCLALHQKTHIGEKPYTCKECGQAFSVRSTLTN HQVIHSDK
3896	A	202	498	MVQSCSAYGCKNRYDKDKPVSFHKFPLTRPSLC KEWEAAVRRKNFKPTKYSSICSEHFTPDCFKREC NNKLLKENAVPTIFLCTEPHDKKEDLLEPQEQ
3897	A	2	382	SHGLSRAPHLSAAPAPALASRPCFSSAPCSQGGG GGGPATMIHFILLFSRQGKLRLQKWYITLPDKER KKITREIVQIILSRGHRTSSFVDWKELKLVYKRYA SLYFCCAIE\NQDNELLTLENVHR
3898	A	718	305	SEQEPLLGDTPGSREWDILETEEHYKSRWRSIRIL YLTMFLSSVGFSVVMMSIWPYLQKIDPTADTSFL GWVIASYSLGQMVASPIFGLWSNYRPRKEPLIVSI LISVAANCLYAYLHIPASHNKYYMLVARGLLGIG
3899	A	24	718	FRGRPGIPEREGKGNHSFVEVARVIVVDLHSRLG GAMAERKGTAKVDFLKKIEKEIQQKWDTERVFE VNASNLEKQTSKGKYFVTFPYPYMNGRLHLGHT FSLSKCEFAVGYQRLKGKCCLFPFGLHCTGMPIK ACADKLKREIELY/GCPPDFPDEEEEEEETSVKTE DIIIKDKAKGKKSKAA/AKAGSSKYQWGIMKSLG LSDEEIVKFSEAEHWLDYFNALAIQDLKRMG
3900	A	360	1	VPATSSNVSPSSSESSEPDLSSRSSSSDAPSSSPSVP SPCSLSLSSPESPLLPTLLSSKSPAGSAGPTCGCPS GPGLRATA/PSRLSSSIAAH/SSSAPETSRPAAARE RSPPLHDRESHE
3901	A	193	345	GEWAVPPAPGGQGVSIPHGPEPGQGSGVHIAPRQ GEGSDRTEPLICPKAAP

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3902	A	1188	1389	NPAARSAAAREGSPALPPPPVS/SSSGLGLLLPLSP PGSHAANPALSPRAPHSHYRPRPRCGPRRRPR
3903	A	63	396	NNMRNPHLSSNHYLNLARTETVFARMESVKQRI LAPGKEGLKNFAGKSLGQIYRVLEKKQDTGETIE LTEDGKPL*VPERKAPLCDCTCFGLPRRYIIAIMS GLGFCISFG
3904	A	732	1046	AMSECPLILYIHKHIDTYSQSYLFNDLFYPVYSGG RMVTYEHLREVVFGKSEDEHYPLW*VLFGK*YA VAPNALMFIRFM*NCTFVPKLP*VMDLK**LQYK SR
3905	A	46	910	QPPPPPPPPPSPPPPPFPPARALSHLRLHPDACLFPS PFPLPCSTMPGMMEKGPELLGKNRSANGSAKSP AGGGGSGASSTNGGLHYSEPESGCSSDDEHDVG MRVGAEYQARIPEFDPGATKYTDKDNGGMLVW SPYHSIPDAKLDEYIAIAKEKHGYNVEQALGMLF WHKHNIEKSLADLPNFTPFPDEWTVEDKVLFEQ AFSFHGKSFHRIQQMLPDKTIASLVKYYYSWKK TRSRTSLMDRQARKLANRHNQGDSDDDVEETHP MDGNDSDYDPKKEAKKEGMS
3906	A	2	513	KVCNCCSQELETSFTYVDKNINLEQRNRSSPSAK GHNHPGELGWENPNEWSQEAAISLISEEEDDTSS EATSSGKSIDYGFISAILFLVTGILLVIISYIVPREV TVDPNTVAAREMERLEKESARLGAHLDRCVIAG LCLLTLGGVILSCLLMMSMWKGELYRRNRFAS
3907	A	71	412	ILIMSNCLQNFLKITSTRLLCSRLCQQLRSKRKFF GTVPISRLHRRVVITGIGLVTPLGVGTHLVWDRLI GGESGIVSLVGEEYKSIPCSVAAYVPRGSDEGQF NEQNFVSKSD
3908	A	77	746	LGTLLGWRAPLFSRCLAFHSPFILLNTPKLVKTAE LPPDRNYVLGAHPHGIMCTGFLCNFSTESNGFSQ LFPGLRPWLAVLAGLFYLPVYRDYIMSFGLCPVS RQSLDFILSQPQLGQAVVIMVGGAHEALYSVPGE HCLTLQKRKGFVRLALRHGASLVPVYSFGENDIF RLKAFATGSWQHWCQLTFKKLMGFSPCIFWGR GLFSATSWGLLPFAVPITTV
3909	A	1	793	FRAAGRPAAAMGDIPVVGLSSWKASPGKVTEAV KEAIDAGYRHFDCAYFYHNEREVGAGIRCKIKE GAVRREDLLIATKLWCTCHKKSLVETACRKSLK ALKLNYLDLYLIHWPMGFKPPHPEWIMSCSELSF CLSHPRVQDLPLDESNMVIPSDTDFLDTWEAME DLVITGLVKNIGVSNFNHEQLERLLNKPGLRFKP LTNQIECHPYLTQKNLISFCQSRDVSVTAYRPLG GSCEGVDLIDNPVIKRIAKEHGKSPAQILI
3910	A	202	705	FFTMHRKKVDNRIRILIENGVAERQRSLFVVVGD RGKDQVVILHHMLSKATVKARPSVLWCYKKEL GFSSHRKKRMRQLQKKIKNGTLNIKQDDPFELFI AATNIRYCYYNETHKILGNTFGMCVLQDFEALTP NLLARTVETVEGGGLVVILLRTMNSLKQLYTVT M
3911	A	3	723	AGRGARAAGEGGGPFKSRPRPLPSSRSLPAVGGG RYGADKMAAGGAVAAAPECRLLPYALHKWSSF SSTYLPENILVDKPNDQSSRWSSESNYPPQYLILK LERPAIVQNITFGKYEKTHVCNLKKFKVFGGMN EENMTELLSSGLKNDYNKETFTLKHKIDEQMFPC RFIKIVPLLSWGPSFNFSIWYVELSGIDDPDIVQPC

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				LNWYSKYREQEAIRLCLKHFRQHNYTEAFESLQ KKT
3912	A	2	461	FEKKQLRRPSLFLLGCCSFGIMAPSLWKGLEGIG LFALAHAAFSAAQHRSYMRLTEKEDESLPIDIVL QTLLAFAVTCYGIVHIAGEFKDMDATSELKNKTF DTVRNHPSFYVFNHRGSEYFSGPSDTANSSNQDA LSSNTSLKLRKLESLRR
3913	A	362	20	APGRPEAKVPERSRESGSRRVRGPLLQLRPGRTS RPASGRGRGGAGGSYGKMRKPDSKIVLLGDMN VGKTSLLQRYMERRFPDTVSTVGGAFYLKQWRS YNISIWDTAGEAGAA
3914	A	1	7545	PGIRVGITSQTGLSSNLQENCSKLAFISSHGTEKQ LQCMPMEGRGRASSSISDLQGKGFEKGTGEKHV PGVGSARHSPQASAGGSPWQRGKAQTRWLGKP DPGRKRRRGSPQEEGGLRVSAAARLLCSGANRC KVLVRQNSTPNTQQPAVHPSTPPSRPLPQAGRCL VAPLRPHPDWVAAKTLAKALRAPGKPWRLAAP SPLGDLGAPGLPGPSTAPRTLSVEEPGVECNQLC LYADVTDPVLCLGQKDPGVEGKHCEKEKISSSK ELKHVHAKSEPSKPARRLSESLHVVDENKNESKI EREHKRRTSTPVIMEGVQEETDTRDVKRQVERSE ICTEEPQKQKSTLKNEKHLKKDDSETPHLKSLLK KEVKSSKEKPEREKTPSEDKLSVKHKYKGDCMH KTGDETELHSSEKGLKVEENIQKQSQQTKLSSDD KTERKSKHRNERKLSVLGKDGKPVSEYIIKTDEN VRKENNKKERRLSAEKTKAEHKSRRSSDSKIQK DSLGSKQHGITLQRRSESYSEDKCDMDSTNMDS NLKPEEVVHKEKRRTKSLLEEKLVLKSKSKTQG KQVKVVETELQEGATKQATTPKPDKEKNTEEND SEKQRKSKVEDKPFEETGVEPVLETASSSAHSTQ KDSSHRAKLPLAKEKYKSDKDSTSTRLERKLSD GHKSRSLKHSSKDIKKKKDENKSDDKDGKEVDSS HEKARGNSSLMEKKLSRRLCENRRGSLSQEMAK GEEKLAANTLSTPSGSSLQRPKKSGDMTLIPEQEP MEIDSEPGVENVFEVSKTQDNRNNNSHQDIDSEN MKQKTSATVQKDELRTCTADSKATAPAYKPGR GTGVNSNSEKHADHRSTLTKKMHIQSAVSKMNP GEKEPIHRGTTEVNIDSETVHRMLLSAPSENDRV QKNLKNTAAEEHVAQGDATLEHSTNLDSSPSLSS VTVVPLRESYDPDVIPLFDKRTVLEGSTASTSPAD HSALPNQSLTVRESEVLKTSDSKEGGEGFTVDTP AKASITSKRHIPEAHQATLLDGKQGKVIMPLGSK LTGVIVENENITKEGGLVDMAKKENDLNAEPNL KQTIKATVENGKKDGIAVDHVVGLNTEKYAETV KLKHKRSPGKVKDISIDVERRNENSEVDTSAGSG SAPSVLHQRNGQTEDVATGPRRAEKTSVATSTE GKDKDVTLSPVKAGPATTTSSETRQSEVALPCTS IEADEGLIIGTHSRNNPLHVGAEASECTVFAAAEE GGAVVTEGFAESETFLTSTKEGESGECAVAESED RAADLLAVHAVKIEANVNSVVTEEKDDAVTSAG SEEKCDGSLSRDSEIVEGTITFISEVESDGAVTSAG TEIRAGSISSEEVDGSQGNMMRMGPKKETEGTV TCTGAEGRSDNFVICSVTGAGPREERMVTGAGV VLGDNDAPPGTSASQEGDGSVNDGTEGESAVTS TGITEDGEGPASCTGSEDSSEGFAISSESEENGESA

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				MDSTVAKEGTNVPLVAAGPCDDEGIVTSTGAKE EDEEGEDVVTSTGRGNEIGHASTCTGLGEESEGV LICESAEGDSQIGTVVEHVEAEAGAAIMNANENN VDSMSGTEKGSKDTDICSSAKGIVESSVTSAVSG KDEVTPVPGGCEGPMTSAASDQSDSQLEKVEDT TISTGLVGGSYDVLVSGEVPECEVAHTSPSEKED EDIITSVENEECDGLMATTASGDITNQNSLAGGK NQGKVLIISTSTTNDYTPQVSAITDVEGGLSDALR TEENMEGTRVTTEEFEAPMPSAVSGDDSQLTASR SEEKDECAMISTSIGEEFELPISSATTIKCAESLQP VAAAVEERATGPVLISTADFEGPMPSAPPEAESP LASTSKEEKDECALISTSIAEECEASVSGVVVESE NERAGTVMEEKDGSGIISTSSVEDCEGPVSSAVP QEEGDPSVTPAEEMGDTAMISTSTSEGCEAVMIG AVLQDEDRLTITRVEDLSDAAIISTSTAECMPISA SIDRHEENQLTADNPEGNGDLSATEVSKHKVPM PSLIAENNCRCPGPVRGGKEPGPVLAVSTEEGHN GPSVHKPSAGQGHPSAVCAEKEEKHGKECPEIGP FAGRGQKESTLHLINAEEKNVLLNSLQKEDKSPE TGTAGGSSTASYSAGRGLEGNANSPAHLRGPEQ TSGQTAKDSSVSSIRYLAAVNTGAIKADDMPPVQ GTVAEHSFLPAEQQGSEDNLKTSTTKCITGQESKI APSHTMIPPATYSVALLAPKCEQDLTIKNDYSGK WTDQASAEKTGDDNSTRKSFPEEGDIMVTVSSE ENVCDIGNEESPLNVLGGLKLKANLKMEAYVPS EEEKNGEILAPPESLCGGKPSGIAELQREPLLVNE SLNVENSGFRTNEEIHSESYNKGEISSGRKDNAE AISGHSVEADPKEVEEEERHMPKRKRKQHYLSSE DEPDDNPDVLDSRIETAQRQCPETEPHATKEENS RDLEELPKTSSETNSTTSRVMEEKDEYSSSETTGE KPEQNDDDTIKSQE
3915	A	1	7545	PGIRVGITSQTGLSSNLQENCSKLAFISSHGTEKQ LQCMPMEGRGRASSSISDLQGKGFEKGTGEKHV PGVGSARHSPQASAGGSPWQRGKAQTRWLGKP DPGRKRRRGSPQEEGGLRVSAAARLLCSGANRC KVLVRQNSTPNTQQPAVHPSTPPSRPLPQAGRCL VAPLRPHPDWVAAKTLAKALRAPGKPWRLAAP SPLGDLGAPGLPGPSTAPRTLSVEEPGVECNQLC LYADVTDPVLCLGQKDPGVEGKHCEKEKISSSK ELKHVHAKSEPSKPARRLSESLHVVDENKNESKI EREHKRRTSTPVIMEGVQEETDTRDVKRQVERSE ICTEEPQKQKSTLKNEKHLKKDDSETPHLKSLLK KEVKSSKEKPEREKTPSEDKLSVKHKYKGDCMH KTGDETELHSSEKGLKVEENIQKQSQQTKLSSDD KTERKSKHRNERKLSVLGKDGKPVSEYIIKTDEN VRKENNKKERRLSAEKTKAEHKSRRSSDSKIQK DSLGSKQHGITLQRRSESYSEDKCDMDSTNMDS NLKPEEVVHKEKRRTKSLLEEKLVLKSKSKTQG KQVKVVETELQEGATKQATTPKPDKEKNTEEND SEKQRKSKVEDKPFEETGVEPVLETASSSAHSTQ KDSSHRAKLPLAKEKYKSDKDSTSTRLERKLSD GHKSRSLKHSSKDIKKKDENKSDDKDGKEVDSS HEKARGNSSLMEKKLSRRLCENRRGSLSQEMAK GEEKLAANTLSTPSGSSLQRPKKSGDMTLIPEQEP MEIDSEPGVENVFEVSKTQDNRNNNSHQDIDSEN

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				MKQKTSATVQKDELRTCTADSKATAPAYKPGR GTGVNSNSEKHADHRSTLTKKMHIQSAVSKMNP GEKEPIHRGTTEVNIDSETVHRMLLSAPSENDRV QKNLKNTAAEEHVAQGDATLEHSTNLDSSPSLSS VTVVPLRESYDPDVIPLFDKRTVLEGSTASTSPAD HSALPNQSLTVRESEVLKTSDSKEGGEGFTVDTP AKASITSKRHIPEAHQATLLDGKQGKVIMPLGSK LTGVIVENENITKEGGLVDMAKKENDLNAEPNL KQTIKATVENGKKDGIAVDHVVGLNTEKYAETV KLKHKRSPGKVKDISIDVERRNENSEVDTSAGSG SAPSVLHQRNGQTEDVATGPRRAEKTSVATSTE GKDKDVTLSPVKAGPATTTSSETRQSEVALPCTS IEADEGLIIGTHSRNNPLHVGAEASECTVFAAAEE GGAVVTEGFAESETFLTSTKEGESGECAVAESED RAADLLAVHAVKIEANVNSVVTEEKDDAVTSAG SEEKCDGSLSRDSEIVEGTITFISEVESDGAVTSAG TEIRAGSISSEEVDGSQGNMMRMGPKKETEGTV TCTGAEGRSDNFVICSVTGAGPREERMVTGAGV VLGDNDAPPGTSASQEGDGSVNDGTEGESAVTS TGITEDGEGPASCTGSEDSSEGFAISSESEENGESA MDSTVAKEGTNVPLVAAGPCDDEGIVTSTGAKE EDEEGEDVVTSTGRGNEIGHASTCTGLGEESEGV LICESAEGDSQIGTVVEHVEAEAGAAIMNANENN VDSMSGTEKGSKDTDICSSAKGIVESSVTSAVSG KDEVTPVPGGCEGPMTSAASDQSDSQLEKVEDT TISTGLVGGSYDVLVSGEVPECEVAHTSPSEKED EDIITSVENEECDGLMATTASGDITNQNSLAGGK NQGKVLIISTSTTNDYTPQVSAITDVEGGLSDALR TEENMEGTRVTTEEFEAPMPSAVSGDDSQLTASR SEEKDECAMISTSIGEEFELPISSATTIKCAESLQP VAAAVEERATGPVLISTADFEGPMPSAPPEAESP LASTSKEEKDECALISTSIAEECEASVSGVVVESE NERAGTVMEEKDGSGIISTSSVEDCEGPVSSAVP QEEGDPSVTPAEEMGDTAMISTSTSEGCEAVMIG AVLQDEDRLTITRVEDLSDAAIISTSTAECMPISA SIDRHEENQLTADNPEGNGDLSATEVSKHKVPM PSLIAENNCRCPGPVRGGKEPGPVLAVSTEEGHN GPSVHKPSAGQGHPSAVCAEKEEKHGKECPEIGP FAGRGQKESTLHLINAEEKNVLLNSLQKEDKSPE TGTAGGSSTASYSAGRGLEGNANSPAHLRGPEQ TSGQTAKDSSVSSIRYLAAVNTGAIKADDMPPVQ GTVAEHSFLPAEQQGSEDNLKTSTTKCITGQESKI APSHTMIPPATYSVALLAPKCEQDLTIKNDYSGK WTDQASAEKTGDDNSTRKSFPEEGDIMVTVSSE ENVCDIGNEESPLNVLGGLKLKANLKMEAYVPS EEEKNGEILAPPESLCGGKPSGIAELQREPLLVNE SLNVENSGFRTNEEIHSESYNKGEISSGRKDNAE AISGHSVEADPKEVEEEERHMPKRKRKQHYLSSE DEPDDNPDVLDSRIETAQRQCPETEPHATKEENS RDLEELPKTSSETNSTTSRVMEEKDEYSSSETTGE KPEQNDDDTIKSQE
3916	A	2	773	GPFGVLWPSAKPGPVTAVEARPPDASDPEGLRG GSPAPLLAPGPLDPSGRLHPAVSMMSYLKQPPYG MNGLGLAGPAMDLLHPSVGYPATPRKQRRERTT FTRSQLDVLEALFAKTRYPDIFMREEVALKINLPE

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				SRVQVWFKNRRAKCRQQQQSGSGTKSRPAKKK SSPVRESSGSESSGQFTPPAVSSSASSSSSASSSSA NPAAAAAAGLVVAKLPCPLHIFSLCVFIEENRLV SGSWARDIRSVEETDKSGYR
3917	A	2	776	RNIPGRRFRPPGLRRLLKGPHMPREPRGYRTRVP ALRELVPSSHAGSGASEHCQNNRQGSRQHRASR NVQAGGALAPPRHLCGLCSRLHFLKPDLSVRAA PSRAGASVMALRKELLKSIWYAFTALDVEKSGK VSKSQLRVLSHNLYTVLHIPHDPVALEEHFRDDD DGPVSSQGYMPYLNKYILDKVEEGAFVKEHFDE LCWTLTAKKNYRADSNGNSMLSNQDAFRLWCL FNFLSEDKYPLIMDPDEGEYLLKRYS
3918	A	10	318	WQDLVCLGGSRAQEQKPLQQLWNAILLVAMLL CTGLVVQAQRQASRQSQRELGGQVDLFKRRVV RRLASLKTRRCRLSRAAQGLPDPGAETCAVCLD YFCNKQ
3919	A	1	204	RVLTAINHTLKENLRKFYKGKKDKPLDLRPKKT RAMRRRLNMHEENLKTKKQHRKERLYPLRKYA AKA
3920	A	1	654	RCCRSFVAPLQEKVVFGLFFLGAILCLSFSWLFHT VYCHSEGVSRLFSKLDYSGIALLIMGSFVPWLYY SFYCNPQPCFIYLIVICVLGIAAIIVSQWDMFATPQ YRGVRAGVFLGLGLSGIIPTLHYVISEGFLKAATI GQIGWLMLMASLYITGAALYAARIPERFFPGKCD IWFHSHQLFHIFVVAGAFVHFHGVSNLQEFRFMI GGGCSEEDAL
3921	A	1587	452	LERDGCGGEEGGSVRSGAGPDSDPRGASSPPAG HRGTAASPRPVAAPSRTPAPPHTRARASPGLPSG PAWRRVQWFSRVSGQVSTLMKATVLMRQPGRV QEIVGALRKGGGDRLQVISDFDMTLSRFAYNGK RCPSSYNILDNSKIISEECRKELTALLHHYYPIEID PHRTVKEKLPHMVEWWTKAHNLLCQQKIQKFQI AQVVRESNAMLREGYKTFFNTLYHNNIPLFIFSA GIGDILEEIIRQMKVFHPNIHIVSNYMDFNEDGFL QGFKGQLIHTYNKNSSACENCGYFQQLEGKTNV ILLGDSIGDLTMADGVPGVQNILKIGFLNDKVEE RRERYMDSYDIVLEKDETLDVVNGLLQHILCQG VQLEMQGP
3922	A	2	164	GKIYQRAFGGHSLKFGKGVQAHGCCCVADRTG HSILHTSYGRERPAPVHLRQDT
3923	A	2	3258	EHATHAYAKLGTRRRHREVTVFVPTWQLKKNR RVRESHFLTKLHSLKMLSITPSQLENGKKITTYD YRFMVKLAEETDGIIVTNEQIHILMNSSKKLMVK DRLLPFTFAGNLFMVPDDPLGRDGPTLDEFLKKP NRLDTDIGNFLKVWKTLPPSSASVTELSDDADSG PLESLPNMEEVREEKEERQDEEQRQGQGTQKAA EEDDLDSSLASVFRVECPSLSEEILRCLSLHDPPD GALDIDLLPGAASPYLGIPWDGKAPCQQVLAHL AQLTIPSNFTALSFFMGFMDSHRDAIPDYEALVG PLHSLLKQKPDWQWDQEHEEAFLALKRALVSAL CLMAPNSQLPFRLEVTVSHVALTAILHQEHSGRK HPIAYTSKPLLPDEESQGPQSGGDSPYAVAWALK HFSRCIGDTPVVLDLSYASRTTADPEVREGRRVS KAWLIRWSLLVQDKGKRALELALLQGLLGENRL LTPAASMPRFFQVLPPFSDLSTFVCIHMSGYCFYR

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				EDEWCAGFGLYVLSPTSPPVSLSFSCSPYTPTYA HLAAVACGLERFGQSPLPVVFLTHCNWIFSLLWE LLPLWRARGFLSSDGAPLPHPSLLSYIISLTSGLSS LPFIYRTSYRGSLFAVTVDTLAKQGAQGGGQWW SLPKDVPAPTVSPHAMGKRPNLLALQLSDSTLAD IIARLQAGQKLSGSSPFSSAFNSLSLDKESGLLMF KGDKKPRVWVVPTQLRRDLIFSVHDIPLGAHQR PEETYKKLRLLGWWPGMQEHVKDYCRSCLFCIP RNLIGSELKVIESPWPLRSTAPWSNLQIEVVGPVT ISEEGHKHVLIVADPNTRWVEAFPLKPYTHTAVA QVLLQHVFARWGVPVRLEAAQGPQFARHVLVS CGLALGAQVASLSRDLQFPCLTSSGAYWEFKRA LKEFIFLHGKKWAASLPLLHLAFRASSTDATPFK VLTGGESRLTEPLWWEMSSANIEGLKMDVFLLQ LVGELLELHWRVADKASEKAENRRFKRESQEKE WNVGDQVLLLSLPRNGSSAKWVGPFYIGDRLSL SLYRIWGFPTPEKLGCIYPSSLMKAFAKSGTPLSF KVLEQ
3924	A	1	1826	MGSVTVRYFCYGCLFTSATWTVLLFVYFNFSEV TQPLKNVPVKGSGPHGPSPKKFYPRFTRGPSRVL EPQFKANKIDDVIDSRVEDPEEGHLKFSSELGMIF NERDQELRDLGYQKHAFNMLISDRLGYHRDVPD TRNAACKEKFYPPDLPAASVVICFYNEAFSALLR TVHSVIDRTPAHLLHEIILVDDDSDFDDLKGELDE YVQKYLPGKIKVIRNTKREGLIRGRMIGAAHATG EVLVFLDSHCEVNVMWLQPLLAAIREDRHTVGC PVIDIISADTLAYSSSPVVRGGFNWGLHFKWDLV PLSELGRAEGATAPIKSPTMAGGLFAMNRQYFH ELGQYDSGMDIWGGENLEISFRIWMCGGKLFIIP CSRVGHIFRKRRPYGSPEGQDTMTHNSLRLAHV WLDEYKEQYFSLRPDLKTKSYGNISERVELRKKL GCKSFKWYLDNVYPEMQISGSHAKPQQPIFVNR GPKRPKVLQRGRLYHLQTNKCLVAQGRPSQKG GLVVLKACDYSDPNQIWIYNEEHELVLNSLLCLD MSETRSSDPPRLMKCHGSGGSQQWTFGKNNRLY QVSVGQCLRAVDPLGQKGSVAMAICDGSSSQQ WHLEG
3925	A	5386	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSL VTTQRKLKAMSLLGSRNQLARAVLNPNPMDFCT KDLLTTTSERIIAYLRDFNEDQKKAIETAYAMVK HSPSVAKICLIHGPPGTGKSKTIVGLLYRLLTENQ RKGHSDENSNAKIKQNRVLVCAPSNAAVDELM KKIILEFKEKCKDKKNPLGNCGDINLVRLGPEKSI NSEVLKFSLDSQVNHRMKKELPSHVQAMHKRK EFLDYQLDELSRQRALCRGGREIQRQELDENISK VSKERQELASKIKEVQGRPQKTQSIIILESHIICCT LSTSGGLLLESAFRGQGGVPFSCVIVDEAGQSCEI ETLTPLIHRCNKLILVGDPKQLPPTVISMKAQEYG YDQSMMARFCRLLEENVEHNMISRLPILQLTVQ YRMHPDICLFPSNYVYNRNLKTNRQTEAIRCSSD WPFQPYLVFDVGDGSERRDNDSYINVQEIKLVM EIIKLIKDKRKDVSFRNIGIITHYKAQKTMIQKDL DKEFDRKGPAEVDTVDAFQGRQKDCVIVTCVRA NSIQGSIGFLASLQRLNVTITRAKYSLFILGHLRTL MENQHWNQLIQDAQKRGAIIKTCDKNYRHDAV

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				KILKLKPVLQRSLTHPPTIAPEGSRPQGGLPSSKL DSGFAKTSVAASLYHTPSDSKEITLTVTSKDPERP PVHDQLQDPRLLKRMGIEVKGGIFLWDPQPSSPQ HPGATPPTGEPGFPVVHQDLSHVQQPAAVVAAL SSHKPPVRGEPPAASPEASTCQSKCDDPEEELCH RREARAFSEGEQEKCGSETHHTRRNSRWDKRTL EQEDSSSKKRKLL
3926	A	99	284	MPREDRATWKSNYFLKIIQLLDDYPKRFIVGANN VGSKQMQQIRMSLRGKAVVLMGKNTMMR
3927	A	542	2	AHLLMLNLAL\TDLL\YLTSLPFLIHYYASGENWI FGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIH PMSCFSIHKTRCAVVACAVVWIISLVAVIPMTFLI TSTNRTNRSACLDLTSSDELNTIKWYNLILTA\LL CLPLVIVTLCYTTIIHTLTHGHAN\DSCLKQKARR LTILLL
3928	A	1	1516	GEEAVGGGAEGGGFGVGAQGRAGGRGVEAGR MRLSKTLVDMDMADYSAALDPAYTTLEFENVQ VLTMGNDTSPSEGTNLNAPNSLGVSALCAICGDR ATGKHYGASSCDGCKGFFRRSVRKNHMYSCRFS RQCVVDKDKRNQCRYCRLKKCFRAGMKKEAV QNERDRISTRRSSYEDSSLPSINALLQAEVLSRQIT SPVSGINGDIRAKKIASIADVCESMKEQLLVLVE WAKYIPGFCELPLDDQGALLRAHAGEHLLLGAT KRSMVFKDVLLLGNDYIVPRHCPELAEMSRVSIR ILDELVLPFQELQIDDNEYAYLKAIIFFDPDAKGL SDPGKIKRLRSQVQVSLEDYINDRQYDSRGRFGE LLLLLPTLQSITWQMIEQIQFIKLFGMAKIDNLLQ EMLLGGSPSDAPHAHHPLHPHLMQEHMGTNVIV ANTMPTHLSNGQMCEWPRPRGQAATPETPQPSP PGASGSEPYKLLPGAVATIVKPLSAIPQPTITKQE VI
3929	A	1	2782	RVLSLESPLEKDPRVLGAQSVPRGRALKGLSPLG LDSAFRLFPDPRAGPWNTAVLSSGMEPETALWG PDLQGPEQSPNDAHRGAESENEEESPRQESSGEEI IMGDPAQSPESKDSTEMSLERSSQDPSVPQNPPTP LGHSNPLDHQIPLDPPAPEVVPTPSDWTKACEAS WQWGALTTWNSPPVVPANEPSLRELVQGRPAG AEKPYICNECGKSFSQWSKLLRHQRIHTGERPNT CSECGKSFTQSSHLVQHQRTHTGEKPYKCPDCG KCFSWSSNLVQHQRTHTGEKPYKCTECEKAFTQ STNLIKHQRSHTGEKPYKCGECRRAFYRSSDLIQ HQATHTGEKPYKCPECGKRFGQNHNLLKHQKIH AGEKPYRCTECGKSFIQSSELTQHQRTHTGEKPY ECLECGKSFGHSSTLIKHQRTHLREDPFKCPVCG KTFTLSATLLRHQRTHTGERPYKCPECGKSFSVS SNLINHQRJHRGERPYICADCGKSFIMSSTLIRHQ RIHTGEKPYKCSDCGKSFIRSSHLIQHRRTHTGEK PYKCPECGKSFSQSSNLITHVRTHMDENLFVCSD CGKAFLEAHELEQHRVIHERGKTPARRAQGDSL LGLGDPSLLTPPPGAKPHKCLVCGKGFNDEGIFM QHQRIHIGENPYKNADGLIAHAAPKPPQLRSPRL PFRGNSYPGAAEGRAEAPGQPLKPPEGQEGFSQR RGLLSSKTYICSHCGESFLDRSVLLQHQLTHGNE KPFLFPDYRIGLGEGAGPSPFLSGKPFKCPECKQS FGLSSELLLHQKVHAGGKSSHKSPELGKSSSVLL

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				EHLRSPLGARPYRCSDCRASFLDRVALTRHQETH TQEKPPNPEDPPPEAVTLSTDQEGEGETPTPTESS SHGEGQNPKTLVEEKPYLCPECGAGFTEVAALLL HRSCHPGVSL
3930	A	513	273	KTQETHIYISEHIFFPFLQGFGNLPICMAKTDLSLS HQPDKKGVPSDFILPISDVRASIGAGFIYPLVGTG SRESPLWL
3931	A	16	305	KRRDFLSCWPAFTVLGEARGDQVDWSKLYRDT GLVKMSRKPRASSPFSNNHPSTPKRRGRGKHPLI PGPEALSKFPRQPIREKGPVKEVPGTKGSP
3932	A	16	305	KRRDFLSCWPAFTVLGEARGDQVDWSKLYRDT GLVKMSRKPRASSPFSNNHPSTPKRRGRGKHPLI PGPEALSKFPRQPIREKGPVKEVPGTKGSP
3933	A	1	1546	STHASEHWDSALQLAKHLAPDQIPFISKEYAIQLE FAGDYVNALAHYEKGITGDNKEHDEACLAGVA QMSIRMGDIRRGVNQALKHPSRVLKRDCGAILE NMKQFSEAAQLYEKGLYYDKAASVYIRSKNWA KVGDLLPHVSSPKIHLQYAKAKEADGRYKEAVV AYENAKQWQSVIRIYLDHLNNPEKAVNIVRETQ SLDGAKMVARFFLQLGDYGSAIQFLVMSKCNNE AFTLAQQHNKMEIYADIIGSEDTTNEDYQSIALY FEGEKRYLQAGKFFLLCGQYSRALKHFLKCPSSE DNVAIEMAIETVGQAKDELLTNQLIDHLLGEND GMPKDAKYLFRLYMALKQYREAAQTAIIIAREE QSAGNYRNAHDVLFSMYAELKSQKIKIPSEMAT NLMILHSYILVKIHVKNGDHMKGARMLIRVANN ISKFPSHIVPILTSTVIECHRAGLKNSAFSFAAML MRPEYRSKIDAKYKKKIEGMVRRPDISEIEEATTP CPFCKFLLPESELL
3934	A	334	1268	PTRRPILPLTSPKAISVPSPLQGKQHTLVKSCLSVS GIGGFLVSLSSRMKLQTLAVSVTALKFWSAYVP CQTQDRDALRLTLEQIDLIRRMCASYSELELVTS AKALNDTQKLACLIGVEGGHSLDNSLSILRTFYM LGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL TDFGEKVVAEMNRLGMMVDLSHVSDAVARRAL EVSQAPVIFSHSAARGVCNSARNVPDDILQLLEE ERWAFVMVSLFHGELIQWQPIRPMCSTVADHFD HIKAV\IGSKFIGIGGDYDGAGKYRKKTTCKAPW RTSSRMSS
3935	A	1	883	HETTPAVVQSVLLERGWNKFDKQEQNAEDWNL YWRTSSFRMTEHNSVKPWQQLNHHPGTTKLTR KDCLAKHLKHMRRMYGTSLYQFIPLTFVMPNDY TKFVAEYFQERQMLGTKHSYWICKPAELSRGRG ILIFSDFKDFIFDDMYIVQKYISNPLLIGRYKCDLR IYVCVTGFKPLTIYVYQEGLVRFATEKFDLSNLQ NNYAHLTNSSINKSGASYEKIKEVIGHGCKWTLS RFFSYLRSWDVDDLLLWKKIHRMVILTILAIAPS VPFAANCFELFGFDILIDDNEFHRTG
3936	A	203	441	HLAHSLGPLPKHYQYCVRYLYYQVTKDVIKEFA DDGVKYLELRSTPRRENATGMTKKTYVESILEGI KQSKQENLDIDV

TABLE 7

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (MAXIMUM SCORE)	MeanS (Mean Score)
1	19	0.930	0.680
2	24	0.964	0.863
3	21	0.990	0.901
4	19	0.981	0.942
5	22	0.991	0.928
6	21	0.956	0.843
8	22	0.913	0.718
9	17	0.997	0.969
11	19	0.930	0.680
13	36	0.983	0.863
14	28	0.935	0.839
15	21	0.997	0.955
16	16	0.983	0.944
17	18	0.989	0.884
19	49	0.996	0.719
20	28	0.972	0.920
21	23	0.954	0.905
22	46	0.955	0.568
23	26	0.942	0.654
24	19	0.979	0.941
25	34	0.884	0.565
26	33	0.934	0.584
27	17	0.975	0.914
28	18	0.980	0.934
29	23	0.928	0.718
30	26	0.978	0.885
32	20	0.946	0.719
33	29	0.933	0.671
35	25	0.996	0.920
36	26	0.903	0.579
40	19	0.981	0.942
47	25	0.971	0.909
53	22	0.991	0.928
55	24	0.960	0.808
60	19	0.986	0.967
78	22	0.913	0.718
86	20	0.883	0.555
87	24	0.982	0.889
88	17	0.997	0.969
115	19	0.930	0.680
134	36	0.983	0.863
136	17	0.913	0.696
137	19	0.958	0.905
140	28	0.935	0.839
143	32	0.914	0.740
153	21	0.997	0.955
154	25	0.913	0.583
155	29	0.972	0.857
169	30	0.977	0.817
170	30	0.977	0.819
171	30	0.977	0.819
175	47	0.926	0.606
176	30	0.968	0.872
177	22	0.957	0.791
192	43	0.930	0.678

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (MAXIMUM SCORE)	MeanS (Mean Score)
195	19	0.956	0.860
202	21	0.982	0.871
203	24	0.957	0.870
207	23	0.954	0.905
224	46	0.955	0.568
225	26	0.942	0.654
228	45	0.961	0.839
231	28	0.994	0.937
232	28	0.993	0.896
234	19	0.979	0.942
235	19	0.979	0.941
238	20	0.987	0.943
244	23	0.929	0.683
250	34	0.884	0.565
256	33	0.934	0.584
258	25	0.934	0.729
259	22	0.969	0.871
264	19	0.952	0.753
265	17	0.975	0.914
266	17	0.975	0.914
271	23	0.974	0.884
274	13	0.971	0.834
275	18	0.980	0.934
278	32	0.958	0.668
280	24	0.966	0.881
281	24	0.966	0.881
286	23	0.928	0.718
291	35	0.991	0.824
293	27	0.956	0.806
294	23	0.952	0.827
301	26	0.978	0.885
316	20	0.946	0.719
320	28	0.978	0.726
327	29	0.933	0.671
331	48	0.903	0.571
345	25	0.996	0.920
349	26	0.903	0.579
351	24	0.951	0.876
352	18	0.944	0.716
353	32	0.992	0.854
354	27	0.945	0.817
355	16	0.922	0.716
356	13	0.959	0.818
357	23	0.986	0.878
358	19	0.904	0.671
359	16	0.988	0.951
360	15	0.981	0.938
361	18	0.944	0.716
362	21	0.984	0.869
363	40	0.979	0.813
364	18	0.883	0.693
365	22	0.962	0.908
366	22	0.961	0.827
367	44	0.941	0.624
368	20	0.952	0.791
369	22	0.949	0.840
370	28	0.957	0.682

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (MAXIMUM SCORE)	MeanS (Mean Score)
372	28	0.974	0.894
373	19	0.972	0.947
374	29	0.968	0.785
375	19	0.949	0.897
377	23	0.962	0.910
378	31	0.974	0.895
379	26	0.969	0.939
380	27	0.945	0.817
383	27	0.945	0.817
384	25	0.992	0.877
385	32	0.983	0.825
386	44	0.924	0.564
387	26	0.971	0.894
388	19	0.989	0.862
389	24	0.990	0.947
390	34	0.942	0.635
391	16	0.922	0.716
394	19	0.987	0.970
398	36	0.992	0.866
404	13	0.959	0.818
417	23	0.986	0.878
421	19	0.904	0.671
425	28	0.971	0.717
431	16	0.988	0.951
452	18	0.944	0.716
459	21	0.991	0.902
468	21	0.984	0.869
478	40	0.979	0.813
486	18	0.883	0.693
499	22	0.962	0.908
501	19	0.962	0.877
514	44	0.941	0.624
529	20	0.952	0.791
533	39	0.914	0.719
548	28	0.957	0.682
561	28	0.974	0.894
562	28	0.974	0.893
564	18	0.949	0.806
576	19	0.972	0.947
584	29	0.968	0.785
585	28	0.973	0.810
591	19	0.949	0.897
592	24	0.991	0.954
594	20	0.985	0.959
595	20	0.985	0.959
612	23	0.962	0.910
619	31	0.974	0.895
621	15	0.959	0.795
633	26	0.969	0.939
640	20	0.949	0.842
645	25	0.911	0.759
684	25	0.992	0.877
691	32	0.983	0.825
698	44	0.924	0.564
700	19	0.982	0.941
710	26	0.971	0.894
714	23	0.965	0.907

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (MAXIMUM SCORE)	MeanS (Mean Score)
718	19	0.989	0.862
725	21	0.976	0.851
728	33	0.961	0.895
734	25	0.963	0.660
741	34	0.942	0.635
744	19	0.959	0.924
747	16	0.922	0.716
756	26	0.973	0.864
767	22	0.986	0.943
768	27	0.916	0.758
769	19	0.987	0.970
770	22	0.981	0.933
771	34	0.993	0.893
773	20	0.968	0.939
774	21	0.971	0.945
778	22	0.986	0.943
779	32	0.973	0.846
781	23	0.950	0.857
785	27	0.916	0.758
786	27	0.916	0.758
788	22	0.981	0.933
793	22	0.986	0.803
794	39	0.892	0.654
797	27	0.965	0.847
810	22	0.981	0.933
823	34	0.993	0.893
825	17	0.962	0.778
837	20	0.968	0.939
844	25	0.984	0.951
845	17	0.919	0.706
846	21	0.971	0.945
847	21	0.971	0.945
890	22	0.986	0.943
893	24	0.971	0.865
894	24	0.971	0.865
896	32	0.973	0.846
899	31	0.982	0.817
922	15	0.882	0.706
924	21	0.975	0.948
925	21	0.927	0.661
933	20	0.967	0.906
960	20	0.967	0.906
967	38	0.970	0.784
968	47	0.970	0.557
972	36	0.945	0.775

TABLE 8

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
3955	A	235	1272	GPREVLAASSLADGSEEQVMAVALVRERDLSFPG VGDAVVNPTRWHLPAQPEMLYEGGEGRMETLK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				DKTLQELEELQNDSEAIDQLALESPEVQDLQLERE MALATNRSLAERNLEFQGPLEISRSNLSDRYQELR KLVERCQEQKAKLEKFSSALQPGTLLDLLQVEGM KIEEESEAMAEKFLEGEVPLETFLENFSSMRMLSH LRRVRVEKLQEVVRKPRASQELAGDAPPPRSPPP V/PPSPPGNTPCG*RAAAATISHASLPFALQPIPQPA CGPHCPWSPATGPFPSSVPALLLQRASGPHLPGSP AWTQGCCGLLLVPTEEHAAPPYGFPPPPGPAWPG Y
3956	A	821	385	SICADRTERVGIFFYIPAGTTDEADVTHP*EGHSYL SNHAGIQRSSRP/SHYQGE/WHDNCFTADELQLLT YQLCHTYVRCTRSVSIPAPAYYAHLVAFRARYHL VDKEHDSAEGSHVSGQSNGRDPQALAKAVQIHQ DTLRTMYFA
3957	A	4621	240	ELISTFKLLLEKKRSEVMKMKKRYEVGLEKLDSA SSQVATMQMELEALHPQLKVASKEVDEMMIMIE KESVEVAKTEKIVKADETIANEQAMASKAIKDEC DADLAGALPILESALAALDTLTAQDITVVKSMKSP PAGVKLVMEAICILKGIKADKIPDPTGSGKKIEDF WGPAKRLLGDMRFLQSLHEYDKDNIPPAYMNIIR KNYIPNPDFVPEKIRNASTAAEGLCKWVIAMDSY DKVAKIVAPKKIKLAAAEGELKIAMDGLRKKQA ALKEVQDKLARLQDTLELNKQKKADLENQVDLC SKKLERAEQLIGGLGGEKTRWSHTALELGQLYIN LTGDILISSGVVAYLGAFTSTYRQNQTKEWTTLCK GRDIPCSDDCSLMGTLGEAVTIRTWNIAGLPSDSF SIDNGIIIMNARRWPLMIDPQSQANKWIKNMEKA NSLYVIKLSEPDYVRTLENCIQFGTPVLLENVGEE LDPILEPLLLKQTFKQGGSTCIRLGDSTIEYAPDFR FYITTKLRNPHYLPETSVKVTLLNFMITPEGMQDQ LLGIVVAQERPDLEEEKQALILQGAENKRQLKEIE DKILEVLSSSEGNILEDETAIKILSSSKALANEISQK QEVAEETEKKIDTTRMGYRPIAIHSSILFFSLADLA NIEPMYQYSLTWFINLFILSIENSEKSEILAKRLQIL KDHFTYSLYVNVCRSLFEKDKLLFSFCLTINLLLH ERAINKAEWRFLLTGGIGLDNPYANPCTWLPQKS WDEICRLDDLPAFKTIRREFMRLKDGWKKVYDSL EPHHEVFPEEWEDKANEFQRMLIIRCLRPDKVIPM LQEFIINRLGRAFIEPPPFDLAKAFGDSNCCAPLIFV LSPGADPMAALLKFADDQGYGGSKLSSLSLGQGQ GPIAMKMLEKAVKEGTWVVLQNCHLATSWMPT LEKVCEELSPESTHPDFRMWLTSYPSPNFPVSVLQ NGVKMTNEAPKGLRANIIRSYLMDPISDPEFFGSC KKPEEFKKLLYGLCFFHALVQERRKFGPLWWNIP YEFNETDLRISVQQLHMFLNQYEELPYEALRYMT GECNYGGRVTDDWDRRTLRSILNKFFNPELVENS DYKFDSSGIYFVPPSGDHKSYIEYTKTLPLTPAPEI FGMNANADITKDQSETQLLFDNILLTQSRSAGAG AKSSDEVVNEVASDILGKLPNNFDIEAAMRRYPT TYTQSMNTVLVQEMGRFNKLLKTIRDSCVNIQKA IKGLAVMSTDLEEVVSSILNVKIPEMWMGKSYPS LKPLGSYVNDFLARLKFLQQWYEVGPPPVFWLSG FFFTQAFLTGAQQNYARKYTIPIDLLGFDYEVMED KEYKHPPEDGVFIHGLFLDGASWNRKIKKLAESH PKILYDTVPVMWLKPCKRADIPKRPSYVAPLYKT

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				SERRGVLSTTGHSTNFVIA\MTLPSDQPKEHWIGR GVALLCQLNS
3958	A	35	529	GADMAKSKNHTTHNQSRKWHRNVIKKPLSQRYK SLKGVDPKFLGNMCFTKKHKKKGLKKMQADSA KAVSTCAKAIEALVKPKEVKPKIPKGVSCELN*LA YIAYPKFWTCACACIAKGLRLCQPKAKAQDQTK AQVQIKAQAAAPASVPTQAPKGAQAPTKASG
3959	A	1883	763	LLVLLLRTNLLIASSTRISRATLTCSPPGIPVDPRVR PRVRSHLVMYLGITTGSLHKAVVSGDSSAHLVEEI QLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPR ANCSVYESCVDCVLARDPHCAWDPESRTCCLLSA PNLNSWKQDMERGNPEWACASGPMSRSLRPQSR PQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAA VPEASSTVYNGSLLLIVQDGVGGLYQCWATENGF SYPVISYWVDSQDQTLALDPELAGIPREHVKVPLT RVSGGAALAAQQSYWPHFVTVTVLFALVLSGALI ILVASPLRALRARGKVQGCETLRPGEKAPLSREQH LQSPKECRTSASDVDADNNCLGTEVA
3960	A	1	481	SYAAPSLFVKSLYWALAFMAVLLAVSGVVIVVLA SRAGARCQQCPPGWVLSEEHCYYFSAEAQAWEA SQAFCSAYHATLPLLSHTQDFLGRYPVSRHSWVG AWRGPQGWHWIDEAPLPPQLLPEDGEDNLDINCG ALEEGTLVAANCSTPRPWVCAKGTQ

TABLE 9

SEQ ID NO:	Accession Number	Species	Description	Smith Waterman Score	% Identity
3937	Y27700	Homo sapiens	Human secreted protein encoded by gene No. 12.	193	25
3938	AF093097	Homo sapiens	putative RNA-binding protein Q99	3881	84
3939	AB012308	Anthocidaris crassispina	B2HC	4169	74
3940	U10248	Homo sapiens	ribosomal protein L29	787	95
3941	Y99418	Homo sapiens	Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.	4031	100
3942	AL023516	Gallus gallus	B locus C type Lectin	198	35

5

TABLE 10

SEQ ID NO:	Accession No.	Description	Results*
3937	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.168e-11 209-224
3942	BL00615	C-type lectin domain proteins.	BL00615A 16.68 6.400e-11 37-55

* Results Include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence

● ●

TABLE 11

SEQ ID NO:	PFAM Name	Description	P-Value	PFAM Score
3938	Piwi	Piwi domain	2.6e-150	512.7
3940	Ribosomal_L29e	Ribosomal L29e protein family	2.3e-19	77.8
3941	Sema	Sema domain	4e-181	615.1
3942	lectin_c	Lectin C-type domain	0.086	-7.1

5

TABLE 12

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (Maximum Score)	Means (Mean Score)
3941	31	0.985	0.926
3942	21	0.974	0.894

TABLE 13

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SEQ ID NO: of full length nucleotide sequence	SEQ ID NO: of full length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority Docket number corresponding SEQ ID NO: in priority application	SEQ ID NO: in USSN 09/496,914
3937	3943	3949	3955	787CIP2G_1	787_3587
3938	3944	3950	3956	787CIP2G_2	787_3813
3939	3945	3951	3957	787CIP2G_3	787_4462
3940	3946	3952	3958	787CIP2G_4	787_4887
3941	3947	3953	3959	787CIP2G_5	787_5794
3942	3948	3954	3960	787CIP2G_6	787_8743

TABLE 14

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	ABD003	3940
adult brain	Clontech	ABR006	3940
adult brain	Invitrogen	ABR014	3940
cultured preadipocytes	Strategene	ADP001	3937
adult heart	GIBCO	AHR001	3940
adult kidney	GIBCO	AKD001	3940
adult lung	GIBCO	ALG001	3940
young liver	GIBCO	ALV001	3940
adult ovary	Invitrogen	AOV001	3938, 3940-3941
adult spleen	GIBCO	ASP001	3940-3941
testis	GIBCO	ATS001	3940
bone marrow	Clontech	BMD001	3938, 3940
bone marrow	Clontech	BMD004	3940
adult cervix	BioChain	CVX001	3940
endothelial cells	Strategene	EDT001	3940
fetal brain	Clontech	FBR006	3940
fetal brain	Invitrogen	FBT002	3940-3941
fetal heart	Invitrogen	FHR001	3940
fetal kidney	Clontech	FKD001	3940
fetal kidney	Clontech	FKD002	3940

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
fetal liver-spleen	Columbia University	FLS001	3937, 3940
fetal liver-spleen	Columbia University	FLS002	3938, 3941
fetal liver-spleen	Columbia University	FLS003	3940
fetal liver	Clontech	FLV004	3940
fetal skin	Invitrogen	FSK001	3940-3942
fetal spleen	BioChain	FSP001	3940
fetal brain	GIBCO	HFB001	3937, 3940-3941
infant brain	Columbia University	IB2002	3937, 3939, 3941
leukocyte	GIBCO	LUC001	3940-3941
leukocyte	Clontech	LUC003	3940-3941
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	3940
mammary gland	Invitrogen	MMG001	3937, 3940-3941
neuronal cells	Strategene	NTU001	3937, 3942
prostate	Clontech	PRT001	3938
rectum	Invitrogen	REC001	3940
salivary gland	Clontech	SALs03	3941
small intestine	Clontech	SIN001	3940
skeletal muscle	Clontech	SKM001	3940
spinal cord	Clontech	SPC001	3940
thymus	Clontech	THMc02	3938
thyroid gland	Clontech	THR001	3942
uterus	Clontech	UTR001	3940

WHAT IS CLAIMED IS:

1.   An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-984, 1969-2952, 3937-3942 or 3949-3954, a full length protein coding portion of SEQ ID NO:1-984, 1969-2952, 3937-3942 or 3949-3954, a mature protein coding portion of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, an active domain coding portion of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, and complementary sequences thereof.

2.   An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3.   An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4.   The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5.   An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6.   A vector comprising the polynucleotide of claim 1.

7.   An expression vector comprising the polynucleotide of claim 1.

8.   A host cell genetically engineered to comprise the polynucleotide of claim 1.

9.   A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10.   An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
        (a)   a polypeptide encoded by any one of the polynucleotides of claim 1; and
        (b)   a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954.

11.   A composition comprising the polypeptide of claim 10 and a carrier.

12.   An antibody directed against the polypeptide of claim 10.

13.   A method for detecting the polynucleotide of claim 1 in a sample, comprising:

        a)   contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

        b)   detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14.   A method for detecting the polynucleotide of claim 1 in a sample, comprising:

        a)   contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

        b)   amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

        c)   detecting said product and thereby the polynucleotide of claim 1 in the sample.

15.   The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16.   A method for detecting the polypeptide of claim 10 in a sample, comprising:

        a)   contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

        b)   detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17.   A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

        a)   contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

        b)   detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected fromm the group consisting of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, a mature protein coding portion of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, an active domain coding portion of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO: 985-1968, 2953-3936, 3943-3948 or 3955-3960, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26.   The collection of claim 22, wherein the collection is provided in a computer-readable format.

27.   A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28.   A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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Lys Ser Ile Leu Phe Val Pro Thr Ser Ala Pro Arg Gly Leu Phe Asp
            385                 390                 395

gaa tat gga tct aaa aag agc gat tac att aag ctc tat gtg cgc cgt       1426
Glu Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr Val Arg Arg
400                 405                 410                 415

gta ttc atc aca gac gac ttc cat gat atg atg cct aaa tac ctc aat       1474
Val Phe Ile Thr Asp Asp Phe His Asp Met Met Pro Lys Tyr Leu Asn
                    420                 425                 430

ttt gtc aag ggt gtg gtg gac tca gat gat ctc ccc ttg aat gtt tcc       1522
Phe Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Val Ser
                435                 440                 445

cgc gag act ctt cag caa cat aaa ctg ctt aag gtg att agg aag aag       1570
Arg Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val Ile Arg Lys Lys
                450                 455                 460

ctt gtt cgt aaa acg ctg gac atg atc aag aag att gct gat gat aaa       1618
Leu Val Arg Lys Thr Leu Asp Met Ile Lys Lys Ile Ala Asp Asp Lys
            465                 470                 475

tac aat gat act ttt tgg aaa gaa ttt ggt acc aac atc aag ctt ggt       1666
Tyr Asn Asp Thr Phe Trp Lys Glu Phe Gly Thr Asn Ile Lys Leu Gly
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8

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          480                    485                    490                    495

gtg att gaa gac cac tcg aat cga aca cgt ctt gct aaa ctt ctt agg      1714
Val Ile Glu Asp His Ser Asn Arg Thr Arg Leu Ala Lys Leu Leu Arg
                500                    505                    510

ttc cag tct tct cat cat cca act gac att act agc cta gac cag tat      1762
Phe Gln Ser Ser His His Pro Thr Asp Ile Thr Ser Leu Asp Gln Tyr
                515                    520                    525

gtg gaa aga atg aag gaa aaa caa gac aaa atc tac ttc atg gct ggg      1810
Val Glu Arg Met Lys Glu Lys Gln Asp Lys Ile Tyr Phe Met Ala Gly
                530                    535                    540

tcc agc aga aaa gag gct gaa tct tct cca ttt gtt gag cga ctt ctg      1858
Ser Ser Arg Lys Glu Ala Glu Ser Ser Pro Phe Val Glu Arg Leu Leu
                545                    550                    555

aaa aag ggc tat gaa gtt att tac ctc aca gaa cct gtg gat gaa tac      1906
Lys Lys Gly Tyr Glu Val Ile Tyr Leu Thr Glu Pro Val Asp Glu Tyr
560                    565                    570                    575

tgt att cag gcc ctt ccc gaa ttt gat ggg aag agg ttc cag aat gtt      1954
Cys Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val
                580                    585                    590

gcc aag gaa gga gtg aag ttc gat gaa agt gag aaa act aag gag agt      2002
Ala Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser
                595                    600                    605

cgt gaa gca gtt gag aaa gaa ttt gag cct ctg ctg aat tgg atg aaa      2050
Arg Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys
                610                    615                    620

gat aaa gcc ctt aag gac aag att gaa aag gct gtg gtg tct cag cgc      2098
Asp Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg
                625                    630                    635

ctg aca gaa tct ccg tgt gct ttg gtg gcc agc cag tac gga tgg tct      2146
Leu Thr Glu Ser Pro Cys Ala Leu Val Ala Ser Gln Tyr Gly Trp Ser
640                    645                    650                    655

ggc aac atg gag aga atc atg aaa gca caa gcg tac caa acg ggc aag      2194
Gly Asn Met Glu Arg Ile Met Lys Ala Gln Ala Tyr Gln Thr Gly Lys
                660                    665                    670

gac atc tct aca aat tac tat gcg agt cag aag aaa aca ttt gaa att      2242
Asp Ile Ser Thr Asn Tyr Tyr Ala Ser Gln Lys Lys Thr Phe Glu Ile
                675                    680                    685

aat ccc aga cac ccg ctg atc aga gac atg ctt cga cga att aag gaa      2290
Asn Pro Arg His Pro Leu Ile Arg Asp Met Leu Arg Arg Ile Lys Glu
                690                    695                    700

gat gaa gat gat aaa aca gtt ttg gat ctt gct gtg gtt ttg ttt gaa      2338
Asp Glu Asp Asp Lys Thr Val Leu Asp Leu Ala Val Val Leu Phe Glu
                705                    710                    715

aca gca acg ctt cgg tca ggg tat ctt tta cca gac act aaa gca tat      2386
Thr Ala Thr Leu Arg Ser Gly Tyr Leu Leu Pro Asp Thr Lys Ala Tyr
720                    725                    730                    735

gga gat aga ata gaa aga atg ctt cgc ctc agt ttg aac att gac cct      2434
Gly Asp Arg Ile Glu Arg Met Leu Arg Leu Ser Leu Asn Ile Asp Pro
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9

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                    740                    745                    750

gat gca aag gtg gaa gaa gag cct gaa gaa gaa cct gaa gag aca gca    2482
Asp Ala Lys Val Glu Glu Glu Pro Glu Glu Glu Pro Glu Glu Thr Ala
            755                    760                    765

gaa gac aca aca gaa gac aca gag caa gac gaa gat gaa gaa atg gat    2530
Glu Asp Thr Thr Glu Asp Thr Glu Gln Asp Glu Asp Glu Glu Met Asp
            770                    775                    780

gtg gga aca gat gaa gaa gaa gaa aca gca aag gaa tct aca gct gaa    2578
Val Gly Thr Asp Glu Glu Glu Glu Thr Ala Lys Glu Ser Thr Ala Glu
        785                    790                    795

aaa gat gaa ttg taa attatactct caccatttgg atcctgtgtg gagagggaat    2633
Lys Asp Glu Leu  *
800

gtgaaattta catcatttct ttttgggaga gacttgtttt ggatgccccc taatcccctt    2693

ctcccctgca ctgtaaaatg tgggattatg ggtcacagga aaaagtgggt tttttagttg    2753

aatttttttt aacattcctc atgaatgtaa atttgtacta tttaactgac tattcttgat    2813

gtaaaatctt gtcatgtgta taaaaataaa aaagatccca aat                      2856
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```
ttg cgg aat tcg gca cga ggc cga cta caa cag att gga gcc atg gct    48
Leu Arg Asn Ser Ala Arg Gly Arg Leu Gln Gln Ile Gly Ala Met Ala
 1               5                  10                     15

ttg gaa cag aac cag tca aca gat tat tat tat gag gaa aat gaa atg    96
Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn Glu Met
            20                  25                     30

aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc aaa gaa    144
Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile Lys Glu
        35                  40                     45

gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc aca ata    192
Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu Thr Ile
    50                  55                     60

gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca att tat    240
Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala Ile Tyr
65                  70                     75                     80

gcc aaa cat taaaaata tctcgacccc taaaagttct gctcacagtc gttatagttt    296
Ala Lys His

tcattgtcac tcaactgcct tataacattg tcaagttctg ccgagccata gacatcatct    356
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10

actccctgat caccagctgc aacatgagca aacgcatgga catcgccatc caagtcaca   415

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aaacccaaac tacatcccca aggtcagggc caggctctgt tgagtaatgc tccccatcac   120

agcacgcagc acaaggctgg ctgtttgaca aatacacaca taaccaaaag acatgtgaat   180

gtggtttccc aactcacttt aaacaaatat tccgggacca acttcaagga cgttctacaa   240

cagaaactgg actgtactct tcacaaacat caatgtcatg aaagacagaa aggctgagga   300

cctgctccaa acgaaggag gctgcagaga ggacaactaa aggcagcgct tgatcctgga   360

ttggatcctg gaccagaaaa acaacggctt tcaaaatcat tattgggaca gttggcaaat   420

ttgaaacagg aactacaaat tagcaactcc tgggctgatc agagaatatt acacatttcc   480

tgaatttgag aactgtacca tgggcatgtg agaggctgtc cctgttcttg ggaaatgttc   540

actaaaacat cttacggata aacgagcatg atgtatacaa ataatcctca aatggttcat   600

ggttcagaga ggataggaag aaacagggt gagggagaag aggagggaac ga   atg   655
                                                                   Met
                                                                     1

aaa gag aaa atg tgg caa aat gtt ctt tgt tgt acc ctt caa act gct   703
Lys Glu Lys Met Trp Gln Asn Val Leu Cys Cys Thr Leu Gln Thr Ala
              5   10   15

gtg att ttg aaa tta ttt caa aat aaa gtt tta aat att tta aaa aat   751
Val Ile Leu Lys Leu Phe Gln Asn Lys Val Leu Asn Ile Leu Lys Asn
          20   25   30

ttt ttt ctt tct ccc ctt gat acc agg aag aat aaa gtt ttt aaa aaa   799
Phe Phe Leu Ser Pro Leu Asp Thr Arg Lys Asn Lys Val Phe Lys Lys
      35   40   45

tgg gca ggt ggg cca ggc gcg gtg gct cac gcc tgt aat ccc agc act   847
Trp Ala Gly Gly Pro Gly Ala Val Ala His Ala Cys Asn Pro Ser Thr
50   55   60   65

ttg gga ggc cga ggc ggg cgg atc aca aag tca gga gat cga gac cat   895
Leu Gly Gly Arg Gly Gly Arg Ile Thr Lys Ser Gly Asp Arg Asp His
                  70   75   80

cct ggc caa cac ggt gaa acc cgg tct cta cta aaa gta caa aaa att   943
Pro Gly Gln His Gly Glu Thr Arg Ser Leu Leu Lys Val Gln Lys Ile
                  85   90   95

11

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agc cag gtg tgg tgg cag atg act gta ggc caa gct aat tgg gag gct        991
Ser Gln Val Trp Trp Gln Met Thr Val Gly Gln Ala Asn Trp Glu Ala
        100             105                 110

gag gca gga gaa tgg tgc gaa ccc ggg gag ggc aga gct tgc agt gag       1039
Glu Ala Gly Glu Trp Cys Glu Pro Gly Glu Gly Arg Ala Cys Ser Glu
        115             120                 125

cca aga tca ccc act gca ctc cag act ggg taa cagagcaa gactcggtct       1090
Pro Arg Ser Pro Thr Ala Leu Gln Thr Gly  *
130             135                 140

caaaaaaaat aataagttac atttaaatgt catatacata tttaagaaaa aaaaaaccaa     1150

gtacttctca tttaagacag agtagaaatt atttaaaatt aggagttggt gtaaaggatg     1210

agctacatat tcaagtcaaa ttatagtaag tattcactat tccactacca aagtaggtca     1270

attatactaa agagaagaaa tctatgtgaa ttgaggcatt ttctcacttt gatatatgtg     1330

aataaatttc aggttgtcta aattcctagg gttatatagt tagaaatata taattctctt     1390

atagacaggt caactagggg aaataagtta gcacaatcat ttgaattggt tgtctacata     1450

ctgggcaggg cttattcctt ttctttagct tctttgcaca tgtaaagcag gccataagat     1510

gtcctgtttt gccatggaca atgcaaccat ttttaggtcg accttgacaa atcacacaag     1570

gttcaatggc attaaggggc aaactagatt ccacactctc ttctttgtct tgggtttctt     1630

ccctttcaaa ctctttcaca tcttcttggc tgctataaat aatgctacta gaagttgatg     1690

gctgagaata gtcttcactt tcttgtgatt gtgaagcttg tgtaattta tcatcatttt      1750

cctcaacaca tgactctctg gaatcattca ctatagtttt tttacaatca ggaacatcaa     1810

agccctcttc agcttgtgtt gagtttttcca gtttggcttt ctcagagatt tcccctttat    1870

ctttcccttt atcttcagga agccaattct cacgaagggc ccaacatctg ttgcaatgtg     1930

atggaagggg gggattcatt tcattgcatg aagtgcattt ccaatagtca gctaaggaaa     1990

tttcaggatc ttcttcaaat gaatctgtat cactctcccc tgcctgatac acagtaactt     2050

gatatacctc atcatcttca tctgagagtt cttgtccttc ttcactaagg ctataatctt     2110

ctgagtcgag agattcaact tcaaattcta cactaaactg atctgaaact gaatcctgat     2170

ccaaccaatc acctgaatgt tcacttacac cagcatcaag atccggattc gatggcgtcc     2230

ctgtagattc actgctactg cttctttcac aacatatctc ccttattaca cacagagcca     2290

ggctttcatc aaaggaaagg gaaatactat cagattgtg gcgttttctt tgtcgttcac      2350

cagataattc atctgaattt tcttctgtct cactaattgc tctccttcta gatgaggtag     2410

atggtctaga aaccaaatgt gaagatgaag gtttctcttc ctgaagctct tgtacaaggt     2470

ccttttgatc actcccacct tcaaggtgac acctgttctc actcacagat gtacctgagt     2530

ccgatgattc ctgctgattg actactacca agttcctgta gatcatggta tatatttcc      2590

tgtgctcttt cacagagaag cttggcacgc caaacaaatc tcctagaaga tcatttgaac    2650
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12

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aatatacaat atgttgttgc ttctcatcat ataatcgttt agtcataata tactggccaa    2710

gataaaaaag aacctctttc atagtataag tgtctttttg tgcaccaaca gactttaata    2770

acttcaaaag caatggcttt ggtctaacca gggtctcttg ttccgaagct ggaatctgtg    2830

aggtggttac agcaccatca gtaggtacag acatgttggt attgcacatt tgcctgctcc    2890

tcaccatccg gggttttcgc gcttggagtc gggggtccct caagactccc cagtttcctt    2950

cacggggact gactactgcg gaagcacgac gccctgggcc tcggggatca ttccactctc    3010

cgggccaggg cactgggcgc tcgtacgcac taatccgggg agggacggtg ctcctggctg    3070

cgaaagcagc aggatctcgg tcagaggggt cgcggccgcc cctcgggctc ggcttcttgc    3130

tccatctttc cgacacacag ggccacacag gccccagaag cagccaagct cgcgcggtgc    3190
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gcggccgccc cggcggctcc tggaaccccg gttcgcggcg atgccagcca ccccagcgaa      60

gccgccgcag ttcagtgctt ggataatttg aaagtacaat agttggtttc cctgtccacc     120

cgccccactt cgcttgccat cacagcacgc ctatcggatg tgagaggaga agtcccgctg     180

ctcgggcact gtctatatac gcctaacacc tacatatatt ttaaaaacat aaatataat     240

taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact    atg cac     296
                                                          Met His
                                                          1
```

```
ttg cga ctg att tct tgg ctt ttt atc att ttg aac ttt atg gaa tac     344
Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met Glu Tyr
        5                  10                  15

atc ggc agc caa aac gcc tcc cgg gga agg cgc cag cga aga atg cat     392
Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His
        20                  25                  30

cct aac gtt agt caa ggc tgc caa gga ggc tgt gca aca tgc tca gat     440
Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp
35                  40                  45                  50

tac aat gga tgt ttg tca tgt aag ccc aga cta ttt ttt gct ctg gaa     488
Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu
                55                  60                  65

aga att ggc atg aag cag att gga gta tgt ctc tct tca tgt cca agt     536
Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser
                70                  75                  80

gga tat tat gga act cga tat cca gat ata aat aag tgt aca aaa tgc     584
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13

```
Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys
        85                  90                  95

aaa gct gac tgt gat acc tgt ttc aac aaa aat ttc tgc aca aaa tgt        632
Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys
        100                 105                 110

aaa agt gga ttt tac tta cac ctt gga aag tgc ctt gac aat tgc cca        680
Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro
115                 120                 125                 130

gaa ggg ttg gaa gcc aac aac cat act atg gag tgt gtc agt att gtg        728
Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val
                135                 140                 145

cac tgt gag gtc agt gaa tgg aat cct tgg agt cca tgc acg aag aag        776
His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys
                150                 155                 160

gga aaa aca tgt ggc ttc aaa aga ggg act gaa aca cgg gtc cga gaa        824
Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu
            165                 170                 175

ata ata cag cat cct tca gca aag ggt aac cta tgt ccc cca aca aat        872
Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn
        180                 185                 190

gag aca aga aag tgt aca gtg caa agg aag aag tgt cag aag gga gaa        920
Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu
195                 200                 205                 210

cga gga aaa aaa gga agg gag agg aaa aga aaa aaa cct aat aaa gga        968
Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly
            215                 220                 225

gaa agt aaa gaa gca ata cct gac agc aaa agt ctg gaa tcc agc aaa        1016
Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys
            230                 235                 240

gaa atc cca gag caa cga gaa aac aaa cag cag cag aag aag cga aaa        1064
Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys
            245                 250                 255

gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta cac tag agg        1112
Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His *
260                 265                 270

gttccatgag attattgtag actcatgatg ctgctatctc aaccagatgc ccaggacagg       1172

tgctctagcc attaggacca caaatggaca tgtcagttat tgctctgtct aaacaacatt       1232

cccagtagtt gctatattct tcatacaagc atagttaaca acaaagagcc aaaagatcaa       1292

agaagggata ctttcagatg gttgtcttgt gtgcttctct gcatttttaa a               1343
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<212> DNA
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<222> (1)..(795)

<400> 7

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atg gat cca acc atc tca acc ttg gac aca gaa ctg aca cca atc aac      48
Met Asp Pro Thr Ile Ser Thr Leu Asp Thr Glu Leu Thr Pro Ile Asn
 1               5                  10                  15

gga act gag gag act ctt tgc tac aag cag acc ttg agc ctc acg gtg      96
Gly Thr Glu Glu Thr Leu Cys Tyr Lys Gln Thr Leu Ser Leu Thr Val
            20                  25                  30

ctg acg tgc atc gtt tcc ctt gtc ggg ctg aca gga aac gca gtt gtg     144
Leu Thr Cys Ile Val Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val
        35                  40                  45

ctc tgg ctc ctg ggc tgc cgc atg cgc agg aac gcc ttc tcc atc tac     192
Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Phe Ser Ile Tyr
    50                  55                  60

atc ctc aac ttg gcc gca gca gac ttc ctc ttc ctc agc ggc cgc ctt     240
Ile Leu Asn Leu Ala Ala Ala Asp Phe Leu Phe Leu Ser Gly Arg Leu
65                  70                  75                  80

ata tat tcc ctg tta agc ttc atc agt atc ccc cat acc atc tct aaa     288
Ile Tyr Ser Leu Leu Ser Phe Ile Ser Ile Pro His Thr Ile Ser Lys
                85                  90                  95

atc ctc tat cct gtg atg atg ttt tcc tac ttt gca ggc ctg agc atg     336
Ile Leu Tyr Pro Val Met Met Phe Ser Tyr Phe Ala Gly Leu Ser Met
            100                 105                 110

ctg agc acc atc agc acc gag cac cgc ctg tcc gtc ctg tgg ccc atc     384
Leu Ser Thr Ile Ser Thr Glu His Arg Leu Ser Val Leu Trp Pro Ile
        115                 120                 125

tgg tac tgc tgc cac tgc ccc aca cac ctg tca gcg gtc atg tgt gtc     432
Trp Tyr Cys Cys His Cys Pro Thr His Leu Ser Ala Val Met Cys Val
    130                 135                 140

ctg ctc tgg gcc ctg tcc ctg ttg cag agc atc ctg gag tgg atg ttc     480
Leu Leu Trp Ala Leu Ser Leu Leu Gln Ser Ile Leu Glu Trp Met Phe
145                 150                 155                 160

tgt agc ttc ctg ttt agt gat gtt gac tct gat aat tgg tgt caa ata     528
Cys Ser Phe Leu Phe Ser Asp Val Asp Ser Asp Asn Trp Cys Gln Ile
                165                 170                 175

tta gat ttc ctc aca gtc gcg tgg ctg att ttt tta atc tgt ggt tct     576
Leu Asp Phe Leu Thr Val Ala Trp Leu Ile Phe Leu Ile Cys Gly Ser
            180                 185                 190

ctg tgg gtt cac cct ggt cct gct gat cag gat cat atg tgg atc ccg     624
Leu Trp Val His Pro Gly Pro Ala Asp Gln Asp His Met Trp Ile Pro
        195                 200                 205

gaa gat acc gct gac cag gct gta tgt gac cat cct gct cac agg gct     672
Glu Asp Thr Ala Asp Gln Ala Val Cys Asp His Pro Ala His Arg Ala
    210                 215                 220

ggt ctt cct cct ctg tgg cct gcc cct cag cat tca gtt ttt cct att     720
Gly Leu Pro Pro Leu Trp Pro Ala Pro Gln His Ser Val Phe Pro Ile
225                 230                 235                 240
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```
ata ctg gat cca cgt gga cag gga agt ctt att ttg tca tgt tca tct        768
Ile Leu Asp Pro Arg Gly Gln Gly Ser Leu Ile Leu Ser Cys Ser Ser
            245                 250                 255   .

agt ttc tat ttt cct gtc cgc tct taa cagca gtgccaaccc catcatttac        820
Ser Phe Tyr Phe Pro Val Arg Ser  *
            260                 265

ttcttcgtgg gctcctttag gcagcgtcaa aataggcaga acctgaagct ggttctccag      880

agggctctgc aggacgcgtc tgaggtggat gaaggtggag ggcagcttcc tgaggaaatc      940

ctggagctgt cgggaagcag attggagcag tga                                   973
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<212> DNA
<213> Homo sapiens

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<222> (217)..(453)

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gtgaacttag aggttgtggg gccgaggggt cgtcttatag ctaccagccc acaggcattt       120

agtctacgtt ggaggtaaac aaatacgggt cctgcttagg agaaaagaaa aacgtcttac       180

agccagtgtc taaactccaa caacggaat gtatca  atg aga cct tgt ata tgg        234
                                        Met Arg Pro Cys Ile Trp
                                        1                   5

ata cac gtg cat tta aaa ccg ccc tgc cgg ctt gta gag ctt ttg ccg        282
Ile His Val His Leu Lys Pro Pro Cys Arg Leu Val Glu Leu Leu Pro
            10                  15                  20

ttc tcc agc gct tta cag ggg tta tcg cac tta agc ctc gga aca act        330
Phe Ser Ser Ala Leu Gln Gly Leu Ser His Leu Ser Leu Gly Thr Thr
            25                  30                  35

tta cca gtg att cta cca gaa agg aat gaa gaa cag aac ctt cag gaa        378
Leu Pro Val Ile Leu Pro Glu Arg Asn Glu Glu Gln Asn Leu Gln Glu
    40                  45                  50

ttg agt cac aat gca gac aaa tat caa atg gga gat tgt tgc aag gaa        426
Leu Ser His Asn Ala Asp Lys Tyr Gln Met Gly Asp Cys Cys Lys Glu
55                  60                  65                  70

gag att gat gat agt att ttc tac tag ccatt gggaagataa aaggagacag        478
Glu Ile Asp Asp Ser Ile Phe Tyr  *
                75

aagattgaag cctttgccag ccattctttc ccttttttgct tccaaactcc tcaactggga       538

accttcatat gtgcagtatt tatattggat catactggtg attataaaag ttcctaggag        598

gctagaagag ccaaccaaca gagaagggaa agcagtctgt t                            639
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16

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<212> DNA
<213> Homo sapiens

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<222> (416)..(2353)

<220>
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ctctggcagc agcggcggcg cggngacccc ngtccctcgg cctccnnttc ccatcccacc         120

tcccgagcct tcctcttccc gcagcacgcc cggcccggcc cggccgtggc cctcctcagt         180

gccggccgcc atggcagagg cgtccggcgc ggggaaaatc tagcccgggg atttcatgcg         240

gcctagctcg gttccgcctc ctcctcgcgc ggccccagcg gctgcccgca ccccagcccc         300

actccgggcc tccgtgtctc tcctgtgatc gcactgacac ggccggggggg ttagaatgga       360

acaaactgaa ggcccgatga gagaaaggga aagttaagga tgctggagca gaaca atg         418
                                                                    Met
                                                                      1


gat ttc tct ttc tct ttc atg caa ggg atc atg gga aac aca att cag          466
Asp Phe Ser Phe Ser Phe Met Gln Gly Ile Met Gly Asn Thr Ile Gln
             5                  10                  15

caa cca cct caa ctc att gac tcc gcc aac atc cgt cag gag gat gcc          514
Gln Pro Pro Gln Leu Ile Asp Ser Ala Asn Ile Arg Gln Glu Asp Ala
         20                  25                  30

ttt gat aac aac agt gac att gct gaa gat ggt ggc cag aca cca tat         562
Phe Asp Asn Asn Ser Asp Ile Ala Glu Asp Gly Gly Gln Thr Pro Tyr
     35                  40                  45

gaa gct act ttg cag caa ggc ttt cag tac cca gct aca aca gaa gat         610
Glu Ala Thr Leu Gln Gln Gly Phe Gln Tyr Pro Ala Thr Thr Glu Asp
 50                  55                  60                  65

ctt cct cca ctc aca aat ggg tat cca tca tca atc agt gtg tat gaa         658
Leu Pro Pro Leu Thr Asn Gly Tyr Pro Ser Ser Ile Ser Val Tyr Glu
                 70                  75                  80

act caa acc aaa tac cag tca tat aat cag tat cct aat ggg tca gcc         706
Thr Gln Thr Lys Tyr Gln Ser Tyr Asn Gln Tyr Pro Asn Gly Ser Ala
                 85                  90                  95

aat ggc ttt ggt gca gtt aga aac ttt agc ccc act gac tat tat cat        754
Asn Gly Phe Gly Ala Val Arg Asn Phe Ser Pro Thr Asp Tyr Tyr His
             100                 105                 110

tca gaa att cca aac aca aga cca cat gaa att ctg gaa aaa cct tcc        802
Ser Glu Ile Pro Asn Thr Arg Pro His Glu Ile Leu Glu Lys Pro Ser
         115                 120                 125
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17

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cct cca cag cca cca cct cct cct tcg gta cca caa act gtg att cca        850
Pro Pro Gln Pro Pro Pro Pro Pro Ser Val Pro Gln Thr Val Ile Pro
130             135             140             145

aag aag act ggc tca cct gaa att aaa cta aaa ata acc aaa act atc        898
Lys Lys Thr Gly Ser Pro Glu Ile Lys Leu Lys Ile Thr Lys Thr Ile
             150             155             160

cag aat ggc agg gaa ttg ttt gag tct tcc ctt tgt gga gac ctt tta       946
Gln Asn Gly Arg Glu Leu Phe Glu Ser Ser Leu Cys Gly Asp Leu Leu
         165             170             175

aat gaa gta cag gca agt gag cac acg aaa tca aag cat gaa agc aga       994
Asn Glu Val Gln Ala Ser Glu His Thr Lys Ser Lys His Glu Ser Arg
         180             185             190

aaa gaa aag agg aaa aaa agc aac aag cat gac tca tca aga tct gaa      1042
Lys Glu Lys Arg Lys Lys Ser Asn Lys His Asp Ser Ser Arg Ser Glu
         195             200             205

gag cgc aag tca cac aaa atc ccc aaa tta gaa cca gag gaa caa aat      1090
Glu Arg Lys Ser His Lys Ile Pro Lys Leu Glu Pro Glu Glu Gln Asn
210             215             220             225

aga cca aat gag agg gtt gac act gta tca gaa aaa cca agg gaa gaa      1138
Arg Pro Asn Glu Arg Val Asp Thr Val Ser Glu Lys Pro Arg Glu Glu
             230             235             240

cca gta cta aaa gag gaa gcc cca gtt cag cca ata cta tct tct gtt      1186
Pro Val Leu Lys Glu Glu Ala Pro Val Gln Pro Ile Leu Ser Ser Val
             245             250             255

cca aca acg gaa gtg tcc act ggt gtt aag ttt cag gtt ggc gat ctt      1234
Pro Thr Thr Glu Val Ser Thr Gly Val Lys Phe Gln Val Gly Asp Leu
             260             265             270

gtg tgg tcc aag gtg gga acc tat cct tgg tgg cct tgt atg gtt tca      1282
Val Trp Ser Lys Val Gly Thr Tyr Pro Trp Trp Pro Cys Met Val Ser
275             280             285

agt gat ccc cag ctt gag gtt cat act aaa att aac aca aga ggt gcc      1330
Ser Asp Pro Gln Leu Glu Val His Thr Lys Ile Asn Thr Arg Gly Ala
290             295             300             305

cga gaa tat cat gtc cag ttt ttt agc aac cag cca gag agg gcg tgg      1378
Arg Glu Tyr His Val Gln Phe Phe Ser Asn Gln Pro Glu Arg Ala Trp
             310             315             320

gtt cat gaa aaa cgg gta cga gag tat aaa ggt cat aaa cag tat gaa      1426
Val His Glu Lys Arg Val Arg Glu Tyr Lys Gly His Lys Gln Tyr Glu
             325             330             335

gaa tta ctg gct gag gca acc aaa caa gcc agc aat cac tct gag aaa      1474
Glu Leu Leu Ala Glu Ala Thr Lys Gln Ala Ser Asn His Ser Glu Lys
         340             345             350

caa aag att cgg aaa ccc cga cct cag aga gaa cgt gct cag tgg gat      1522
Gln Lys Ile Arg Lys Pro Arg Pro Gln Arg Glu Arg Ala Gln Trp Asp
         355             360             365

att ggc att gcc cat gca gag aaa gca ttg aaa atg act cga gaa gaa      1570
Ile Gly Ile Ala His Ala Glu Lys Ala Leu Lys Met Thr Arg Glu Glu
370             375             380             385
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18

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aga ata gaa cag tat act ttt att tac att gat aaa cag cct gaa gag      1618
Arg Ile Glu Gln Tyr Thr Phe Ile Tyr Ile Asp Lys Gln Pro Glu Glu
                390                 395                 400

gct tta tcc caa gca aaa aag agt gtt gcc tcc aaa acc gaa gtt aaa      1666
Ala Leu Ser Gln Ala Lys Lys Ser Val Ala Ser Lys Thr Glu Val Lys
                    405                 410                 415

aaa acc cga cga cca aga tct gtg ctg aat act cag cca gaa cag acc      1714
Lys Thr Arg Arg Pro Arg Ser Val Leu Asn Thr Gln Pro Glu Gln Thr
                420                 425                 430

aat gca ggg gag gtg gcc tcc tca ctc tca agt act gaa att cgg aga      1762
Asn Ala Gly Glu Val Ala Ser Ser Leu Ser Ser Thr Glu Ile Arg Arg
        435                 440                 445

cat agc cag agg cgg cac aca agt gcg gaa gag gaa gag cca ccg cct      1810
His Ser Gln Arg Arg His Thr Ser Ala Glu Glu Glu Glu Pro Pro Pro
450                 455                 460                 465

gtt aaa ata gcc tgg aaa act gcg gca gca agg aaa tcc tta cca gct      1858
Val Lys Ile Ala Trp Lys Thr Ala Ala Ala Arg Lys Ser Leu Pro Ala
                    470                 475                 480

tcc att acg atg cac aaa ggg agc ctg gat ttg cag aag tgt aac atg      1906
Ser Ile Thr Met His Lys Gly Ser Leu Asp Leu Gln Lys Cys Asn Met
                485                 490                 495

tct cca gtt gtg aaa att gaa caa gtg ttt gct ctt cag aat gct aca      1954
Ser Pro Val Val Lys Ile Glu Gln Val Phe Ala Leu Gln Asn Ala Thr
                500                 505                 510

ggg gat ggg aaa ttt atc gat caa ttt gtt tat tca aca aag gga att      2002
Gly Asp Gly Lys Phe Ile Asp Gln Phe Val Tyr Ser Thr Lys Gly Ile
        515                 520                 525

ggt aac aaa aca gaa ata agt gtc agg ggg caa gac agg ctt ata att      2050
Gly Asn Lys Thr Glu Ile Ser Val Arg Gly Gln Asp Arg Leu Ile Ile
530                 535                 540                 545

tct aca cca aac cag aga aat gaa aag cca acg cag agt gta tca tct      2098
Ser Thr Pro Asn Gln Arg Asn Glu Lys Pro Thr Gln Ser Val Ser Ser
                550                 555                 560

cct gaa gca aca tct ggt tct aca ggc tca gta gaa aag aag caa cag      2146
Pro Glu Ala Thr Ser Gly Ser Thr Gly Ser Val Glu Lys Lys Gln Gln
                565                 570                 575

aga aga tca att aga act cgt tct gaa tca gag aaa tcc act gag gtt      2194
Arg Arg Ser Ile Arg Thr Arg Ser Glu Ser Glu Lys Ser Thr Glu Val
                580                 585                 590

gtg cca aag aag aag atc aaa aag gag cag gtt gaa aca gtt cct cag      2242
Val Pro Lys Lys Lys Ile Lys Lys Glu Gln Val Glu Thr Val Pro Gln
                595                 600                 605

gct aca gtg aag act gga tta cag aaa ggg.tcg gcg gac cgg gga gtg      2290
Ala Thr Val Lys Thr Gly Leu Gln Lys Gly Ser Ala Asp Arg Gly Val
610                 615                 620                 625

cag ggc tct gtc aga ttc agt gac agc tcc gtc tcc gca gcg att gag      2338
Gln Gly Ser Val Arg Phe Ser Asp Ser Ser Val Ser Ala Ala Ile Glu
                630                 635                 640
```

19

gaa act gtg gac tga gattcctgta caatttcatc ccagaaactc cagacttgta   2393
Glu Thr Val Asp *
            645

gtctccatgc aagatttctt tgtcggcggc ttgataaaca gtttctttgt tttcgatttt   2453

gatttcgcca atcatcatta ttggcatttt cctgcctggt ttcttcttca agactctgaa   2513

caattgcttt aacagtcaaa tgattttttt ttttcggttt gagctggatg ggtacagctt   2573

aaatcatggg tccagcctaa aaaccaccat ttaacttaca ctgatcaatt tcaacatgga   2633

ctgtttttgg ttttttgttt ttaaataaag catcattaat gcacatctgc aggggtttgc   2693

caaacagccc aaactgtata cattacaatc attaaaagtt cttatttttt ttaatattag   2753

tgccgttatc atggagaaca gcatgacagc tgtctttggc agtctgtcat ttttctagca   2813

ttttcagaaa ctcatcggaa atggcggtac ctgtgtttcc cttcgaaagc ctctcagtac   2873

agcactcctg ttcctctgtt aaaactcctt gttaatccag tgatcttta ggccaaggaa   2933

atattttgtg atggtgttct gggtccatac accagcaatg aaggagatag atttgtgtac   2993

ttgtgttttt taatcagcat taacatgggc aggcaccctc atttatagat gtcaggaaac   3053

attcagtgaa aaacttgtag aatgggatgt gataacgagg ttccagtaat ctgagcagtc   3113

taacgaggcc cacctcctcc accacagaac gtggctatgt tccaagtgct actctcactc   3173

agcctgttgc ggatcttcat ggcctcagga gacttgtttc tccatgggct cttctggact   3233

gcacacttcc accatagctt gctgggttga tctagatgtc tgtttgttgt atggaaattt   3293

tgggggaaaa aatccaaaac acaaactgtg ggttgaaata ttaaccgtct ccttggttcc   3353

ttggtattca ccgtgcctga tctgcacatt tcatcgtggc tgtttctgta tagcctatac   3413

tgcattagcc caagagattg ttgctttgta acttttgca ctattgtttt ggctggattt   3473

gtattacaca cagtttttaaa aaaaacaatt ccacactaaa aaaaaaaaa   3522

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            <213> Homo sapiens

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            <222> (174)..(1541)

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ctccgggtgc gagagacagg tcgggccccc taggcagcga ccgcagcgc aatcccggcg   120

ctcgcccaag gaccctggaa gctaccgtta ccccgccggg cagcgtgggc gcc   atg   176
                                                             Met
                                                              1

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agc agc tcg gga ctg aat tcg gag aag gta gct gct ctg ata cag aaa        224
Ser Ser Ser Gly Leu Asn Ser Glu Lys Val Ala Ala Leu Ile Gln Lys
              5                   10                  15

ctg aat tcc gac ccc cag ttc gta ctt gcc cag aat gtc ggg acc acc        272
Leu Asn Ser Asp Pro Gln Phe Val Leu Ala Gln Asn Val Gly Thr Thr
              20                  25                  30

cac gac ctg ctg gac atc tgt ctg aag cgg gcc acg gtg cag cgc gcg        320
His Asp Leu Leu Asp Ile Cys Leu Lys Arg Ala Thr Val Gln Arg Ala
          35                  40                  45

cag cat gtg ttc cag cac gcc gtg ccc cag gag ggc aag cca atc acc        368
Gln His Val Phe Gln His Ala Val Pro Gln Glu Gly Lys Pro Ile Thr
50                  55                  60                  65

aac cag aag agc tca ggg cga tgc tgg atc ttt tct tgt ctg aat gtt        416
Asn Gln Lys Ser Ser Gly Arg Cys Trp Ile Phe Ser Cys Leu Asn Val
                  70                  75                  80

atg agg ctt cca ttc atg aaa aag tta aat att gaa gaa ttt gag ttt        464
Met Arg Leu Pro Phe Met Lys Lys Leu Asn Ile Glu Glu Phe Glu Phe
                  85                  90                  95

agc caa tct tac ctg ttt ttt tgg gac aag gtt gaa cgc tgt tat ttc        512
Ser Gln Ser Tyr Leu Phe Phe Trp Asp Lys Val Glu Arg Cys Tyr Phe
              100                 105                 110

ttc ttg agt gct ttt gtg gac aca gcc cag aga aag gag cct gag gat        560
Phe Leu Ser Ala Phe Val Asp Thr Ala Gln Arg Lys Glu Pro Glu Asp
              115                 120                 125

ggg agg ctg gtg cag ttt ttg ctt atg aac cct gca aat gat ggt ggc        608
Gly Arg Leu Val Gln Phe Leu Leu Met Asn Pro Ala Asn Asp Gly Gly
130                 135                 140                 145

caa tgg gat atg ctt gtt aat att gtt gaa aaa tat ggt gtt atc cct        656
Gln Trp Asp Met Leu Val Asn Ile Val Glu Lys Tyr Gly Val Ile Pro
                  150                 155                 160

aag aaa tgc ttc cct gaa tct tat aca aca gag gca acc aga agg atg        704
Lys Lys Cys Phe Pro Glu Ser Tyr Thr Thr Glu Ala Thr Arg Arg Met
              165                 170                 175

aat gat att ctg aat cac aag atg aga gaa ttc tgt ata cga ctg cgg        752
Asn Asp Ile Leu Asn His Lys Met Arg Glu Phe Cys Ile Arg Leu Arg
              180                 185                 190

aac ctg gta cac agt gga gca acc aaa gga gaa atc tcg gcc aca cag        800
Asn Leu Val His Ser Gly Ala Thr Lys Gly Glu Ile Ser Ala Thr Gln
              195                 200                 205

gac gtc atg atg gag gag ata ttc cga gtg gtg tgc atc tgt ttg ggt        848
Asp Val Met Met Glu Glu Ile Phe Arg Val Val Cys Ile Cys Leu Gly
210                 215                 220                 225

aat cca cca gag aca ttc acc tgg gaa tat cga gac aaa gat aaa aat        896
Asn Pro Pro Glu Thr Phe Thr Trp Glu Tyr Arg Asp Lys Asp Lys Asn
                  230                 235                 240

tat cag aaa att ggc ccc ata aca ccc ttg gag ttt tac agg gaa cat        944
Tyr Gln Lys Ile Gly Pro Ile Thr Pro Leu Glu Phe Tyr Arg Glu His
              245                 250                 255
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gtc aag cca ctc ttc aat atg gaa gat aag att tgt tta gtg aat gac          992
Val Lys Pro Leu Phe Asn Met Glu Asp Lys Ile Cys Leu Val Asn Asp
        260             265                 270

cct agg ccc cag cac aag tac aac aaa ctt tac aca gtg gaa tac tta         1040
Pro Arg Pro Gln His Lys Tyr Asn Lys Leu Tyr Thr Val Glu Tyr Leu
        275             280                 285

agc aat atg gtt gga ggg aga aaa act cta tac aac aac cag ccc att         1088
Ser Asn Met Val Gly Gly Arg Lys Thr Leu Tyr Asn Asn Gln Pro Ile
290             295                 300                 305

gac ttc ctg aaa aag atg gtt gct gcc tcc atc aaa gat gga gag gct         1136
Asp Phe Leu Lys Lys Met Val Ala Ala Ser Ile Lys Asp Gly Glu Ala
                310                 315                 320

gtg tgg ttt ggc tgt gat gtt gga aaa cac ttc aat agc aag ctg ggc         1184
Val Trp Phe Gly Cys Asp Val Gly Lys His Phe Asn Ser Lys Leu Gly
                325                 330                 335

ctc agt gac atg aat ctc tat gac cat gag tta gtg ttt ggt gtc tcc         1232
Leu Ser Asp Met Asn Leu Tyr Asp His Glu Leu Val Phe Gly Val Ser
                340                 345                 350

ttg aag aac atg aat aaa gcg gag agg ctg act ttt ggt gag tca ctt         1280
Leu Lys Asn Met Asn Lys Ala Glu Arg Leu Thr Phe Gly Glu Ser Leu
        355                 360                 365

atg acc cac gcc atg acc ttc act gct gtc tca gag aag gat gat cag         1328
Met Thr His Ala Met Thr Phe Thr Ala Val Ser Glu Lys Asp Asp Gln
370                 375                 380                 385

gat ggt gct ttc aca aaa tgg aga gtg gag aat tca tgg ggt gaa gac         1376
Asp Gly Ala Phe Thr Lys Trp Arg Val Glu Asn Ser Trp Gly Glu Asp
                390                 395                 400

cat ggc cac aaa ggt tac ctg tgc atg aca gat gag tgg ttc tct gag         1424
His Gly His Lys Gly Tyr Leu Cys Met Thr Asp Glu Trp Phe Ser Glu
                405                 410                 415

tat gtc tac gaa gtg gtg gtg gac agg aag cat gtc cct gaa gag gtg         1472
Tyr Val Tyr Glu Val Val Val Asp Arg Lys His Val Pro Glu Glu Val
                420                 425                 430

cta gct gtg tta gag cag gaa ccc att atc ctg cca gca tgg gac ccc         1520
Leu Ala Val Leu Glu Gln Glu Pro Ile Ile Leu Pro Ala Trp Asp Pro
        435                 440                 445

atg gga gct ttg gct gag tga ta ctgccctcca gctctttcct ccttccatgg         1573
Met Gly Ala Leu Ala Glu  *
450                 455

aacctgacgt agctgcaaag gacagatcca gggactgaag ccaaagttat gcaagggact     1633

gtgtgttgcc acaggacaca gtcagatttc cagtctccac caggaacctc ttcagaaagt     1693

gtgctttatg ctgaaacaga atactgttaa aggaaaaaaa agaggggga agatcaggtc      1753

atactatcta ctctcctcat ctctaacagc tcaggatctc ttagcatttt aattagatgt     1813

aattgtttgt ctttaactgt caaaaagttt ggttctgtgt ctgtgtttta ataagacgag     1873

aggacgagcg attgaggtgt atggagagaa aacagaccta atgctccttg ttcctagagt     1933
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agagtggagg gagggtggcc taagagttga gctctcggaa ctgcatgctg ctggacagta   1993

tcactgtctt tcctagatgg cagtcactga attccatttt ttcaaggtaa tttcttgtgc   2053

ctctaatagc ccaagaatgg gaggttgatc agatctgaca tgattccttc ctgttctgaa   2113

ctgtggggtg cacatctctg cttgagtcag gtttgagtag aggcttagag acagttgggt   2173

gagaacaacc aaaatcttat catggtctca gtcataatca ttaggggggaa ctctagccaa   2233

atggtttaac ttctgcctgt ggaactgggg attgggtggg caggaaaagg tgatatccat   2293

tctttctgat aactagatgg tgctgagaag cttttgaata aaaactttgc taaatgagaa   2353

taagctgaaa aaa                                                      2366
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<210> 11
<211> 1732
<212> DNA
<213> Homo sapiens

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<222> (241)..(495)

<400> 11
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cacttatgac tccgccggaa aaattacttt aaaaatcgcc aaaaattact tggagcaaag   120

ggcagtccgg cggcgttcgc caaggtggcg cagtcggttt tgacctgtag cagagaacca   180

attctggaga acagcctcac ttctttgatt gaatacttac ataatgcatt ggaacatgac   240
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atg aga tta agg ttt aat aat gat aga atg aag acc aca ata aaa gag      288
Met Arg Leu Arg Phe Asn Asn Asp Arg Met Lys Thr Thr Ile Lys Glu
1               5                   10                  15

acc aca atc ctt agc tca gca att ctt acc ttt ctt acc tat ttg atg      336
Thr Thr Ile Leu Ser Ser Ala Ile Leu Thr Phe Leu Thr Tyr Leu Met
            20                  25                  30

aag atg tct ttt gaa agg tgt act gca agg aac aaa atg ttt gta aat      384
Lys Met Ser Phe Glu Arg Cys Thr Ala Arg Asn Lys Met Phe Val Asn
        35                  40                  45

tct ccc ttt tac cca agg gtg gat aat tac tgt acc tcc tca tgg aaa      432
Ser Pro Phe Tyr Pro Arg Val Asp Asn Tyr Cys Thr Ser Ser Trp Lys
    50                  55                  60

aag ttt tat tta aag tgt tat ttc tca ttg aat act atc aaa aag gaa      480
Lys Phe Tyr Leu Lys Cys Tyr Phe Ser Leu Asn Thr Ile Lys Lys Glu
65                  70                  75                  80

aaa aaa atg acc taa actttgaga tagatttggc tctagtaagt atttagttat      535
Lys Lys Met Thr *
                85
```

```
atcacttgca tatctgggag aagaaataag agactatcat cagtacattc ccatctacta   595

aaaaaattta ttttacacat gtcaagggat tacttataac ttccatttta ttactaatag   655
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23

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cttgaaccct tttaatgaag acctaactcc tccaccagaa atttaagttt atgttcttac   715

tttgtttact tataaaatac atctcaggta tttcggatgt ctttttttt tctaagccta   775

tatgaaatga aaaatatatt ggcaaagtaa atgtttaaac cttttacgtt aaaattactt   835

tgaaagatga aaagttagtg ctgttttgt cacgttatac tgaaattaaa tgtttataat   895

ttatattttg ggtttatgta taaatcatgg aatttatgca aaaatatgag tagtacagat   955

tctcctctaa ttctgtagga ctttgaataa tgtgatattt ttcttataat tggacccttg  1015

tgttttgaag aaatgccaac tgcttgaaga atctccttgt tatttgtatt atttgctata  1075

gggttagatg ttgagaaatt ctgctgacaa aaaattttaa gccagtttta cactaaatgt  1135

tcctcagtct gattaatttg ttattggatg tattctgtat ctttcttttg taatttgtaa  1195

cttttatcca cttagcacga atgattctat taaagaaaat cattaggaag tggtagaaac  1255

tttaaatcgc cccagagttt gcctgtttcc atattttatt atcttataat cttcgggagt  1315

gcttacactt atggagctaa cattttcaga gatacagctt cttatagtaa cactaaaact  1375

ttcttcctct ttggactgaa tacctataat tataactata tggtagttta agtttccttg  1435

tgattagtca aaaataccat tttagtatga agcaatgaag tctattattt gttgtcccat  1495

aattgagaaa gcttaaatac accttttatt aagagtttgt aaattctagc ttagtctaca  1555

cagattttta tatcaatttg tttatatttt tattaatgtc atttctggaa gtgtgaaaat  1615

gttaatgttc aacaagcaac attaaaaata gatttgaaac atttatatat agagaggtac  1675

acatttattt actgtttagg tactgaagat tatcacttaa taaaaaatat atatccc      1732
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        <210> 12
        <211> 2913
        <212> DNA
        <213> Homo sapiens

        <220>
        <221> CDS
        <222> (511)..(2913)

        <400> 12
atgaatatgg acatcaatga ttggtacttc gctactcatc atggtgatat tagcggttct    60

agacatatcc tggatttggg actactaaaa gcgcaaaaga aggcccagag aagggagcac   120

atgctaaaac ttgaggctga gaagaaaaag cttcgaacta tacttcaagt tcagtatgta   180

ttgcagaact tgacacagga gcacgtacaa aaagacttca aggggggttt gaatggtgca   240

gtgtatttgc cttcaaaaga acttgactac ctcattaagt tttcaaaact gacctgccct   300

gaaagaaatg aaagtctgag tgttgaagac cagatggagc agtcatcctt gtactttttgg   360

gacctttttgg aaggtagtga gaaagcagtg gtaggaacga catacaaaca cttgaaggat   420
```

24